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(54) Title: HUMAN ORTHOLOGUES OF WART (57) Abstract <p>The present invention relates in part to hWART nucleic acid molecules. The invention also relates in part to nucleic acid molecules encoding portions of hWART full-length proteins, nucleic acid vectors containing hWART nucleic acid molecules, recombinant cells containing such nucleic acid vectors, polypeptides purified from such recombinant cells, antibodies to such polypeptides, and methods of identifying compounds that modulate the function of an hWART polypeptide. Also disclosed are methods for diagnosing abnormal cell proliferative conditions in an organism using hWART-related molecules or compounds.</p>		

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DESCRIPTION

HUMAN ORTHOLOGUES OF WART

FIELD OF THE INVENTION

The present invention relates in part to protein kinases. In particular, the invention concerns the identification of protein kinase proteins which are human orthologues of the drosophila WART gene (hWART).

BACKGROUND OF THE INVENTION

The following description is provided to aid in understanding the invention, but is not admitted to describe or constitute prior art to the invention.

Cellular signal transduction is a fundamental mechanism whereby extracellular stimuli are relayed to the interior of cells and thereby regulate diverse cellular processes. One of the key biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins. Phosphorylation of polypeptides regulates the activity of mature proteins by altering their structure and function. Phosphate most often resides on the hydroxyl moiety of serine, threonine, or tyrosine amino acids in proteins.

Enzymes that mediate phosphorylation of cellular effectors generally fall into two classes. The first class consists of protein kinases which transfer a phosphate

moiety from nucleotide triphosphates to protein substrates.

The second class consists of protein phosphatases which hydrolyze phosphate moieties from phosphoryl protein substrates. The converse functions of protein kinases and protein phosphatases balance and regulate the flow of signals in signal transduction processes.

Protein kinases are generally divided into two classes: receptor and non-receptor type proteins. Protein kinases may also be divided into three classes based upon the amino acids they act upon: (1) Some catalyze the addition or hydrolysis of phosphate on serine or threonine only; (2) some catalyze the addition or hydrolysis of phosphate on tyrosine only; and (3) some catalyze the addition or hydrolysis of phosphate on serine, threonine, and tyrosine.

Altered protein kinase activity has been associated with multiple abnormal cellular functions, including increased cell proliferation. Increased cell proliferation can result from at least two cellular events: (i) mutation, chromosome translocation, or gene amplification of proto-oncogenes (Bishop, Cell 64: 235-248, 1991), or (ii) inactivation, loss by mutation, chromosomal loss, mitotic recombination, or gene conversion of tumor suppressor genes (Lasko et al., Ann Rev Genet 25: 281-314).

A large number of potential tumor suppressor genes have been isolated from *Drosophila melanogaster*, a species of fruit fly. Watson et al., J. Cell Sci. 18: 19-33 ,

1994. Potential tumor suppressor genes are identified in this organism by first deleting, obstructing, or mutating a gene, and then detecting over-proliferative cell growth of specific tissues in dissected larvae and pupae. Xu et al., Development 121: 1053-1063, 1995. This organism provides an ideal system for identifying potential tumor suppressor genes as it reproduces rapidly and its genome is readily manipulated by persons skilled in the art.

An example of a putative tumor suppressor gene identified in *Drosophila* is the *wts* gene. Loss or inactivation of both copies of the *wts* gene results in the growth of tumors on the legs and wings of the flies.

Bryant et al., Development 1993 Supplement: 239-249, 1993.

The large size of these tumors suggests that the cells undergo more divisions than normal. *Id.* In addition, the rounded shape of the tumors suggests that the division of the mutant cells is not preferentially oriented. *Id.* These observations taken together with the increased thickness of the cuticles around the mutant cells suggest that the *wts* gene regulates cell adhesion, cell contact inhibition, and/or cell boundary recognition in *Drosophila*.

Several of the genes characterized as potential tumor suppressors in *Drosophila* are cloned. In particular, the *wts* gene contains a region that bears sequence similarity to the catalytic regions of mammalian non-receptor serine/threonine protein kinases. Watson, BioEssays 17:

673-676, 1995. However, the human orthologues of the *Drosophila wts* gene have not been reported.

SUMMARY OF THE INVENTION

The invention relates in part to novel human orthologues of the *Drosophila wts* gene (hWARTs). The *Drosophila wts* gene encodes a non-receptor serine/threonine kinase. The properties of the human orthologues are described herein. The present invention concerns polypeptides of hWART, nucleic acids encoding such polypeptides, cells, tissues and animals containing such nucleic acids, antibodies to the polypeptides, assays utilizing the polypeptides, and methods relating to all of the foregoing.

The term "orthologue" as used herein, refers to a gene that is more closely related, in terms of nucleic acid sequence, to another gene than a gene which is a homologue.

In the context of this invention, "homologous" indicates that the nucleotide sequences of two genes and/or the sequences of the gene products (e.g., amino acid sequences) have significant similarity, and that the gene products perform a similar cellular function. Thus, two homologous genes may have sequences which have 50, 60, 70, 80, 90, or greater percent nucleotide sequence identity. By "closely related" in the context of this invention, it is meant nucleic acid sequences that have greater than 90% identity.

The hWARTS genes encode proteins that are potential drug targets for controlling aberrant cell proliferation. Unlike their *Drosophila* ortholog, the hWARTS genes may not function as tumor suppressor genes. While their mRNA is absent from most normal cells they are abundantly expressed in many types of tumor cells. However, based on the high degree of sequence identity in the catalytic and non-catalytic regions between the hWART proteins and the *Drosophila wts*, it is likely that the hWART genes are involved in regulating cell adhesion, cell contact inhibition, and/or cell boundary recognition, and in regulation of signal transduction pathways related to cell proliferation.

Thus, in a first aspect, the invention features an isolated, enriched, or purified nucleic acid molecule encoding an hWART polypeptide.

By "isolated" in reference to nucleic acid it is meant a polymer of 14, 17, 21 or more nucleotides conjugated to each other, including DNA or RNA that is isolated from a natural source or that is synthesized. The isolated nucleic acid of the present invention is unique in the sense that it is not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular (i.e., chromosomal) environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply

that the sequence is the only nucleotide sequence present, but that it is essentially free (about 90 - 95% pure at least) of non-nucleotide material naturally associated with it and thus is meant to be distinguished from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid it is meant that the specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of the total DNA or RNA present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other DNA or RNA present, or by a preferential increase in the amount of the specific DNA or RNA sequence, or by a combination of the two. However, it should be noted that "enriched" does not imply that there are no other DNA or RNA sequences present, just that the relative amount of the sequence of interest has been significantly increased.

The term "significant" here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other nucleic acids of about at least 2 fold, more preferably at least 5 to 10 fold or even more. The term also does not imply that there is no DNA or RNA from other sources. The other source DNA may, for example, comprise DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term distinguishes the sequence from

naturally occurring enrichment events, such as viral infection, or tumor type growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, e.g., in terms of mg/ml). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones can be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an

approximately 10^6 -fold purification of the native message.

Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The term is also chosen to distinguish clones already in existence which may encode hWARTs but which have not been isolated from other clones in a library of clones. Thus, the term covers clones encoding hWART which are isolated from other non-hWART clones.

The term "nucleic acid molecule" describes a polymer of deoxyribonucleotides (DNA) or ribonucleotides (RNA). The nucleic acid molecule may be isolated from a natural source by cDNA cloning or subtractive hybridization or synthesized manually. The nucleic acid molecule may be synthesized manually by the triester synthetic method or by using an automated DNA synthesizer.

The term "cDNA cloning" refers to hybridizing a small nucleic acid molecule, a probe, to genomic cDNA. The probe hybridizes (binds) to complementary sequences of cDNA.

The term "complementary" describes two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. Thus if a nucleic acid sequence contains the following sequence of bases, thymine, adenine, guanine

and cytosine, a "complement" of this nucleic acid molecule would be a molecule containing adenine in the place of thymine, thymine in the place of adenine, cytosine in the place of guanine, and guanine in the place of cytosine. Because the complement can contain a nucleic acid sequence that forms optimal interactions with the parent nucleic acid molecule, such a complement can bind with high affinity to its parent molecule.

The term "hybridize" refers to a method of interacting a nucleic acid sequence with a DNA or RNA molecule in solution or on a solid support, such as nitrocellulose, nylon or some combination of these materials. If a nucleic acid sequence binds to the DNA or RNA molecule with high affinity, it is said to "hybridize" to the DNA or RNA molecule. The strength of the interaction between the probing sequence and its target can be assessed by varying the stringency of the hybridization conditions. Under highly stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having one or two mismatches out of 20 contiguous nucleotides.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. Stringency is controlled by varying salt or denaturant concentrations. Examples of hybridization conditions are shown in the examples

described herein. High stringent conditions may mean conditions that are at least as stringent as the following: hybridization in 50% formamide, 5x SSC, 50 mM NaH_2PO_4 , pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5x Denhart solution at 42 °C overnight; washing with 2x SSC, 0.1% SDS at 45 °C; and washing with 0.2x SSC, 0.1% SDS at 45 °C. Those skilled in the art will recognize how such conditions can be varied to vary specificity and selectivity.

cDNAs are molecules that may be reverse-transcribed from fragments of message RNA from a genomic source. These fragments form a cDNA library of nucleic acid molecules. cDNA libraries are constructed from natural sources such as mammalian blood, semen, or tissue.

The term "subtractive hybridization" refers to a method similar to cDNA cloning except that cDNA prepared from mRNA in unstimulated cells is added to mRNA in stimulated or different types of cells. cDNA/mRNA can then be precipitated to enrich the mRNA specific to the stimulation signal or different cell type.

The term "hWART nucleic acid molecule" as used herein refers to a nucleic acid molecule that encodes an hWART polypeptide. hWART nucleic acid molecules can be identified by hybridization procedures and cloning procedures as described herein.

An hWART polypeptide can be encoded by a full-length nucleic acid sequence or any portion of the full-length

nucleic acid sequence. In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, or SEQ ID NO:2, a nucleic acid sequence that hybridizes to the nucleic acid sequence set forth in SEQ ID NO:1, or SEQ ID NO:2, or a functional derivative (as defined below) of either of the foregoing. The nucleic acid may be isolated from a natural source by cDNA cloning or subtractive hybridization; the natural source may be mammalian (human) blood, semen, or tissue and the nucleic acid may be synthesized by the triester or other method or by using an automated DNA synthesizer.

The term "mammalian" refers to such organisms as mice, rats, rabbits, goats, more preferably monkeys and apes, and most preferably humans.

In other preferred embodiments, the nucleic acid molecule of the invention comprises a nucleotide sequence that (a) encodes a polypeptide having the full length amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring hWART polypeptide; (d) encodes an hWART polypeptide having the full length amino acid sequence of the sequence set forth in SEQ ID NO:3 or SEQ ID NO:4, except that it lacks one or more of the following segments of amino acid residues: 12-45, 55-151, 236-377, 404-520,

555-559, 601-702, 691-998, 1011-1086 of SEQ ID NO:3, or 1-33, 43-139, 342-466, 467-480, 514-518, 974-1048 of SEQ ID NO:4; (e) is the complement of the nucleotide sequence of (d); (f) encodes a polypeptide having the amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4 from amino acid residues 12-45, 55-151, 236-377, 404-520, 555-559, 601-702, 691-998, 1011-1086 of SEQ ID NO:3, or 1-33, 43-139, 342-466, 467-480, 514-518, 974-1048 of SEQ ID NO:4; (g) is the complement of the nucleotide sequence of (f); (h) encodes a polypeptide having the full length amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4, except that it lacks one or more of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, and a C-terminal domain; or (i) is the complement of the nucleotide sequence of (h). The nucleic acid molecule of the invention is isolated, enriched, or purified from, preferably, a mammal, or most preferably from a human.

In yet other preferred embodiments, the nucleic acid is an isolated conserved or unique region, for example those useful for the design of hybridization probes to facilitate identification and cloning of additional polypeptides, or for the design of PCR probes to facilitate cloning of additional polypeptides.

By "conserved nucleic acid regions", it is meant regions present on two or more nucleic acids encoding an hWART polypeptide, to which a particular nucleic acid

sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acids encoding hWARTs polypeptides are provided in Abe, et al. J. Biol. Chem. 19:13361, 1992 (hereby incorporated by reference herein in its entirety, including any drawings). Preferably, conserved regions differ by no more than 5 out of 20 contiguous nucleotides.

By "unique nucleic acid region" it is meant a sequence present in a full length nucleic acid coding for an hWART polypeptide that is not present in a sequence coding for any other known naturally occurring polypeptide. Such regions preferably comprise 14, 17, 21 or more contiguous nucleotides present in the full length nucleic acid encoding an hWART polypeptide. In particular, a unique nucleic acid region is preferably of human origin.

In yet another aspect, the invention relates to a nucleic acid vector comprising a nucleic acid molecule encoding an hWART polypeptide and a promoter element effective to initiate transcription in a host cell.

The term "nucleic acid vector" relates to a single or double stranded circular nucleic acid molecule that can be transfected or transformed into cells and replicate independently or within the host cell genome. A circular double stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes.

An assortment of vectors, restriction enzymes, and the knowledge of the nucleotide sequences that the restriction

enzymes operate upon are readily available to those skilled in the art. A nucleic acid molecule of the invention can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

Many techniques are available to those skilled in the art to facilitate transformation or transfection of the expression construct into a prokaryotic or eukaryotic organism. The terms "transformation" and "transfection" refer to methods of inserting an expression construct into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field, or detergent, to render the host cell outer membrane or wall permeable to nucleic acid molecules of interest.

The term "promoter element" describes a nucleotide sequence that is incorporated into a vector that, once inside an appropriate cell, can facilitate transcription factor and/or polymerase binding and subsequent transcription of portions of the vector DNA into mRNA. The promoter element precedes the 5' end of the hWART nucleic acid molecule such that the latter is transcribed into mRNA. Host cell machinery then translates mRNA into a polypeptide.

Those skilled in the art would recognize that a nucleic acid vector can contain many other nucleic acid elements besides the promoter element and the hWART nucleic acid molecule. These other nucleic acid elements include,

but are not limited to, origins of replication, ribosomal binding sites, nucleic acid sequences encoding drug resistance enzymes or amino acid metabolic enzymes, and nucleic acid sequences encoding secretion signals, periplasm or peroxisome localization signals, or signals useful for polypeptide purification.

The invention also features a nucleic acid probe for the detection of a nucleic acid encoding an hWART polypeptide in a sample.

The term "nucleic acid probe" refers to a nucleic molecule that is complementary to and can bind a nucleic acid sequence encoding the amino acid sequence substantially similar to that set forth in SEQ ID NO:3, or SEQ ID NO:4.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid molecules encoding at least 46 contiguous amino acids of the sequences set forth in SEQ ID NO:3, SEQ ID NO:4, or a functional derivative thereof. Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. Under highly stringent hybridization conditions only highly complementary nucleic acid sequences hybridize.

Preferably, such conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20 contiguous nucleotides.

Methods for using the probes include detecting the presence or amount of hWART RNA in a sample by contacting

the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to hWART RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for an hWART polypeptide may be used in the identification of the sequence of the nucleic acid detected (for example see, Nelson et al., in *Nonisotopic DNA Probe Techniques*, p. 275 Academic Press, San Diego (Kricka, ed., 1992) hereby incorporated by reference herein in its entirety, including any drawings). Kits for performing such methods may be constructed to include a container having disposed therein a nucleic acid probe.

The invention also features a nucleic acid molecule as set forth in SEQ ID NO:1 or SEQ ID NO:2 or fragments thereof, comprising one or more regions that encode an hWART polypeptide or an hWART domain polypeptide, where the hWART polypeptide or the hWART domain polypeptide is fused to a non-WART polypeptide. Such fused polypeptides include, for example, but are not limited to, a GST-fusion protein.

The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence set forth in SEQ ID NO:1, SEQ ID NO:2, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region

functional in a cell, a sequence complimentary to an RNA sequence encoding an hWART polypeptide and a transcriptional termination region functional in a cell.

Another aspect of the invention relates to a recombinant cell or tissue comprising a nucleic acid molecule encoding an hWART polypeptide. The recombinant cell may comprise a nucleic acid molecule encoding either an hWART polypeptide; an hWART domain polypeptide; or an hWART polypeptide or hWART domain polypeptide fused to a non-WART polypeptide.

The term "recombinant organism" refers to an organism that has a new combination of genes or nucleic acid molecules. A new combination of genes or nucleic acid molecules can be introduced to an organism using a wide array of nucleic acid manipulation techniques available to those skilled in the art.

The term "organism" relates to any living being comprised of a least one cell. An organism can be as simple as one eukaryotic cell or as complex as a mammal. Therefore, a recombinant organism can also be a recombinant cell.

The recombinant cell can be a eukaryotic or prokaryotic organism.

The term "eukaryote" refers to an organism comprised of cells that contain a nucleus. Eukaryotes are differentiated from "prokaryotes" which do not have a nucleus and lack other cellular structures found in

eukaryotes, such as mitochondria and endoplasmic reticulum.

Prokaryotes include unicellular organisms, such as bacteria while eukaryotes are represented by yeast, invertebrates, and vertebrates.

The recombinant cell can harbor a nucleic acid vector that is extragenomic. The term "extragenomic" refers to a nucleic acid vector which does not insert into the cell genome. Many nucleic acid vectors are designed with their own origins of replication allowing them to utilize the recombinant cell replication machinery to copy and propagate the vector nucleic acid sequence. These vectors are small enough that they are not likely to harbor nucleic acid sequences homologous to genomic sequences of the recombinant cell. Thus these vectors replicate independently of the host genome and do not recombine with or integrate into the genome.

A recombinant cell can harbor a portion of a nucleic acid vector in an intragenomic fashion. The term "intragenomic" defines a nucleic acid construct that is incorporated within the cell genome. Multiple nucleic acid vectors available to those skilled in the art contain nucleic acid sequences that are homologous to nucleic acid sequences in a particular organism's genomic DNA. These homologous sequences will result in recombination events that integrate portions of the vector into the genomic DNA.

Those skilled in the art can control which nucleic acid sequences of the vector are integrated into the cell genome

by flanking the portion to be incorporated into the genome with homologous sequences in the vector.

Another aspect of the invention features an isolated, enriched, or purified hWART polypeptide.

By "hWART polypeptide" it is meant an amino acid sequence substantially similar to the sequence shown in SEQ ID NO:3, SEQ ID NO:4, or fragments thereof. A sequence that is substantially similar will preferably have at least 90% identity (more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:3 or SEQ ID NO:4.

The hWART polypeptides of the present invention preferably have a substantially similar biological activity to the proteins encoded by the full length nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:2, or to the proteins with amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4. By "biological activity" it is meant an activity of the hWART protein in a cell. The biological activity of the hWART is related to some of the activities of the cell which include, but are not limited to, cell proliferation, motogenesis, metastasis, tumor escape, cell adhesion, transformation, or apoptosis.

By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues in the two sequences by the total number of residues and multiplying the product by 100. Thus, two copies of

exactly the same sequence have 100% identity, but sequences that are less highly conserved and have deletions, additions, or replacements have a lower degree of identity.

Those skilled in the art will recognize that several computer programs are available for determining sequence identity.

By "isolated" in reference to a polypeptide is meant a polymer of 6, 12, 18 or more amino acids conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide it is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total of amino acids present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount

of other amino acids present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that "enriched" does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acids of about at least 2 fold, more preferably at least 5 to 10 fold or even more. The term also does not imply that there is no amino acid from other sources. The other source amino acid may, for example, comprise amino acid encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, e.g., in terms of mg/ml). Purification of at least one order of magnitude, preferably two or three

orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

In another aspect, the invention features an isolated, enriched, or purified hWART polypeptide fragment.

By "hWART polypeptide fragment" it is meant an amino acid sequence that is less than the full-length amino acid sequence. The full-length amino acid sequences of hWART1 and hWART2 are shown in SEQ ID NO:3 and SEQ ID NO:4. Examples of fragments include hWART domains, hWART mutants and hWART-specific epitopes.

By "hWART domain" it is meant a portion of the hWART polypeptide having homology to amino acid sequences from one or more known proteins wherein the sequence predicts some common function, interaction or activity. Well known examples of domains are the SH2 (Src Homology 2) domain (Sadowski, et al, Mol. Cell. Biol. 6:4396, 1986; Pawson and Schlessinger, Curr. Biol. 3:434, 1993), the SH3 domain (Mayer, et al, Nature 332:272, 1988; Pawson and Schlessinger, Curr. Biol. 3:434, 1993), and pleckstrin (PH) domain (Ponting, TIBS 21:245, 1996; Haslam, et al, Nature 363:309, 1993), all of which are domains that mediate protein:protein interaction or protein:lipid interaction, and the kinase catalytic domain (Hanks and Hunter, FASEB J 9:576-595, 1995). Computer programs designed to detect such homologies are well known in the art. The relative

homology is at least 20%, more preferably at least 30% and most preferably at least 35%.

By "hWART mutant" it is meant an hWART polypeptide which differs from the native sequence in that one or more amino acids have been changed, added or deleted. Changes in amino acids may be conservative or non-conservative. By "conservative" it is meant the substitution of an amino acid for one with similar properties such as charge, hydrophobicity, structure, etc. Examples of polypeptides encompassed by this term include, but are not limited to, (1) chimeric proteins which comprise a portion of an hWART polypeptide sequence fused to a non-hWART polypeptide sequence, for example, a polypeptide sequence of hemmagglutinin (HA), (2) hWART proteins lacking a specific domain, for example the catalytic domain, and (3) hWART proteins having a point mutation. An hWART mutant will retain some useful function such as, for example, binding to a natural binding partner, catalytic activity, or the ability to bind to an hWART specific antibody (as defined below).

By "hWART-specific epitope" it is meant a sequence of amino acids that is both antigenic and unique to an hWART polypeptide. An hWART-specific epitope can be used to produce hWART-specific antibodies, as more fully described herein. Particularly preferred epitopes are shown in the Examples section below.

By "recombinant hWART polypeptide" it is meant to include a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (e.g., present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

The polypeptide of the invention comprises an amino acid sequence having (a) the full length amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4; (b) the full length amino acid sequence of the sequence set forth in SEQ ID NO:3 or SEQ ID NO:4, except that it lacks one or more of the following segments of amino acid residues: 12-45, 55-151, 236-377, 404-520, 555-559, 601-702, 691-998, 1011-1086 of SEQ ID NO:3, or 1-33, 43-139, 342-466, 467-480, 514-518, 974-1048 of SEQ ID NO:4; (c) the amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4 from amino acid residues 12-45, 55-151, 236-377, 404-520, 555-559, 601-702, 691-998, 1011-1086 of SEQ ID NO:3, or 1-33, 43-139, 342-466, 467-480, 514-518, 974-1048 of SEQ ID NO:4; or (d) the full length amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4 except that it lacks one or more of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, and a C-terminal domain.

In yet another aspect, the invention features an antibody (e.g., a monoclonal or polyclonal antibody), or

antibody fragment, having specific binding affinity to an hWART polypeptide or hWART polypeptide fragment.

By "specific binding affinity" is meant that the antibody binds to target (hWART) polypeptides with greater affinity than it binds to other polypeptides under specified conditions. Antibodies having specific binding affinity to an hWART polypeptide may be used in methods for detecting the presence and/or amount of an hWART polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the hWART polypeptide. Diagnostic kits for performing such methods may be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope.

The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

The term "polyclonal" refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

"Monoclonal antibodies" are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art. See, for example, Kohler, et al., *Nature* 256:495-497 (1975), and U.S. Patent No. 4,376,110.

The term "antibody fragment" refers to a portion of an antibody, often the hypervariable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hypervariable region is a portion of an antibody that physically binds to the polypeptide target.

In another aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to an hWART polypeptide. By "hybridoma" is meant an immortalized cell line which is capable of secreting an antibody, for example an hWART antibody. In preferred embodiments the hWART antibody comprises a sequence of amino acids that is able to specifically bind an hWART polypeptide.

The invention features a method for identifying human cells containing an hWART polypeptide, or a related sequence. The method involves identifying the novel polypeptide in human cells using techniques that are routine and standard in the art, such as those described

herein for identifying hWART polypeptides (e.g., cloning, Southern or Northern blot analysis, *in situ* hybridization, PCR amplification, etc.).

The invention also features methods of screening cells for natural binding partners of hWART polypeptides. By "natural binding partner" it is meant a protein that interacts with an hWART polypeptide. Binding partners include ligands, agonists, antagonists and downstream signaling molecules such as adaptor proteins and may be identified by techniques well known in the art such as co-immunoprecipitation or by using, for example, a two-hybrid screen. (Fields and Song, U.S. Patent No. 5,283,173, issued February 1, 1994 and, incorporated by reference herein.) The present invention also features the purified, isolated or enriched versions of the polypeptides identified by the methods described above.

In another aspect, the invention provides a method for identifying a substance capable of modulating hWART activity comprising the steps of (a) contacting an hWART polypeptide with a test substance; and (b) determining whether the substance alters the activity of said polypeptide.

The invention also features another method of identifying substances capable of modulating the function of an hWART polypeptide. The method comprises the following steps: (a) expressing an hWART polypeptide in cells; (b) adding a compound to the cells; and (c)

monitoring a change or an absence of a change in cell phenotype, cell proliferation, catalytic activity of the hWART polypeptide, and binding a natural binding partner.

The term "compound" includes small organic molecules including, but not limited to, oxindolinones, quinazolines, tyrphostins, quinoxalines, and those contained within extracts from natural sources. Examples of such compounds are included in section XIII, below.

The term "function" refers to the cellular role of a serine-threonine protein kinase. The serine-threonine protein kinase family includes members that regulate many steps in signaling cascades, including cascades controlling cell growth, migration, differentiation, gene expression, muscle contraction, glucose metabolism, cellular protein synthesis, and regulation of the cell cycle.

The term "modulates" refers to the ability of a compound to alter the function of a protein kinase. A modulator preferably activates the catalytic activity of a protein kinase, more preferably activates or inhibits the catalytic activity of a protein kinase depending on the concentration of the compound exposed to the protein kinase, or most preferably inhibits the catalytic activity of a protein kinase.

The term "catalytic activity" , in the context of the invention, defines the ability of a protein kinase to phosphorylate a substrate. Catalytic activity can be measured, for example, by determining the amount of a

substrate converted to a product as a function of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

The term "substrate" as used herein refers to a molecule that is phosphorylated by or directly interacts with the protein kinase. The substrate is preferably a peptide and more preferably a protein. In relation to the protein kinase RAF, preferred substrates are MEK and the MEK substrate MAPK.

The term "activates" refers to increasing the cellular function of a protein kinase. The protein kinase function is preferably the interaction with a natural binding partner or catalytic activity.

The term "inhibit" refers to decreasing the cellular function of a protein kinase. The protein kinase function is preferably the interaction with a natural binding partner or catalytic activity.

The term "modulates" also refers to altering the function of a protein kinase by increasing or decreasing the probability that a complex forms between a protein kinase and a natural binding partner. A modulator preferably increases the probability that such a complex forms between the protein kinase and the natural binding partner, more preferably increases or decreases the probability that a complex forms between the protein kinase

and the natural binding partner depending on the concentration of the compound exposed to the protein kinase, and most preferably decreases the probability that a complex forms between the protein kinase and the natural binding partner.

The term "complex" refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules bound to one another, either transiently or in succession.

For instance, a receptor protein tyrosine kinase, GRB2, SOS, and RAF sequentially interact in response to a mitogenic ligand.

The term "expressing" as used herein refers to the production of an hWART polypeptide from a nucleic acid vector containing an hWART gene within a cell. The nucleic acid vector is transfected into cells using well known techniques in the art as described herein.

The term "adding" as used herein refers to administering a solution comprising a compound to the medium bathing cells. The solution comprising the compound can also comprise an agent, such as dimethyl sulfoxide, which facilitates the uptake of the compound into the cells.

The term "monitoring" refers to observing the effect of adding the compound to the cells of the method. The effect can be manifested in a change in cell phenotype, cell proliferation, protein kinase catalytic activity, or

in the interaction between a protein kinase and a natural binding partner.

The term "cell phenotype" refers to the outward appearance of a cell or tissue or the function of the cell or tissue. Examples of cell or tissue phenotype are cell size (reduction or enlargement), cell proliferation (increased or decreased numbers of cells), cell differentiation (a change or absence of a change in cell shape), cell survival, apoptosis (cell death), or the utilization of a metabolic nutrient (e.g., glucose uptake).

Changes or the absence of changes in cell phenotype are readily measured by techniques known in the art.

The term "cell proliferation" refers to the rate at which a group of cells divides. The number of cells growing in a vessel can be quantitated by a person skilled in the art when that person visually counts the number of cells in a defined area using a common light microscope. Alternatively, cell proliferation rates can be quantitated by laboratory apparatuses that optically measure the density of cells in an appropriate medium.

The method can utilize any of the molecules disclosed in the invention. These molecules include nucleic acid molecules encoding hWART polypeptides, nucleic acid vectors, recombinant cells, polypeptides, or antibodies of the invention.

Substances identified as modulators of hWART activity can be used to study the effects of hWART modulation in

animal models of cell proliferative disorders. For example, inhibitors of hWART activity can be tested as treatments for cell proliferative disorders such as leukemia or lymphoma using subcutaneous xenograph models in mice.

In a preferred embodiment, the invention provides a method for treating or preventing an abnormal condition by administering a compound which is a modulator of hWART function *in vitro*. The abnormal condition preferably involves abnormality in hWART signal transduction pathway, and most preferably is cancer. Such compounds preferably show positive results in one or more *in vitro* assays for an activity corresponding to treatment of the disease or disorder in question (such as the assays described in example 9 below). Examples of substances that can be screened for favorable activity are provided in section XIII below.

The summary of the invention described above is non-limiting and other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a sequence alignment of the hWART1 and hWART2 amino acid sequences.

Figure 2 is a sequence alignment of the hWART1 and *Drosophila* WART amino acid sequences.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is based in part upon the isolation and characterization of nucleic acid molecules encoding novel hWART proteins. The invention also relates to nucleic acid molecules encoding portions of hWART polypeptides, nucleic acid molecules encoding at least one hWART functional portion, nucleic acid vectors harboring such nucleic acid molecules, recombinant cells containing such nucleic acid vectors, purified polypeptides encoded by such nucleic acid molecules, antibodies to such polypeptides, and methods of identifying compounds that modulate the function of hWART polypeptides. Also disclosed are methods for diagnosing abnormal cell proliferative conditions in an organism.

I. The Nucleic Acids of the Invention.

A. hWART1 Nucleic Acid

The full-length human Wart1 cDNA is 7,382 bp long and consists of a 3,390 bp open reading frame (ORF) flanked by 394 and 3,554 bp of 5' and 3' untranslated regions (UTR) respectively. A 41 nucleotide polyA-rich tail follows the

3' UTR. There are two potential start codons at positions 395 and 431, neither corresponding to the Kozak consensus for initiating methionines. Although the second start site aligns to the N-terminal sequence of the related WART2, we have designated position 395 as the start site since it is the first start site encountered in this extended ORF. There are two additional ATGs located 5' to the start codon at position 395, but they are followed by stop codons after 31 and 10 nucleotides, respectively. The 3,390 nucleotide ORF has the potential to encode a 1,130 amino acid protein.

The 5' untranslated region from nucleotide 12-63 displays 10 copies of the tri-nucleotide repeat, GGC. This repeat is very similar to one found in the human retinoid X receptor beta (BG:M84820). Such repeats have been reported to undergo expansion in various human diseases particularly those associated with neuronal phenotypes. The 3' untranslated region contains an inverted 289 bp Alu-J subfamily repeat (between nucleotides 6,058-6,346). A polyadenylation signal (AATAAA) is found at position 7,338 followed by a 20 nucleotide long polyadenylated stretch.

Sequence analysis of multiple cDNA clones identified three polymorphisms in the human Wart1 gene: (1) at nucleotide 978 resulting in an Ala/Gly change; (2) at nucleotide 1,840, silent; (3) at nucleotides 3,252-3,253 comprising a deletion of two adenosines that results in a C-terminal truncation of the Wart1_h gene, disrupting the putative kinase domain. The frame shift mutation at

position 3252 was observed in two independent clones isolated from the human bone marrow cDNA source. The non-mutated sequence however, was also confirmed in multiple independent clones. Conceivably, truncation of the WART1 STK could play a role in disease progression.

At least 8 EST fragments match the WART1_h gene over its 3' untranslated region and only one (GB:Z16134) was found to span part of the coding region of this gene (nucleotides 2,138-3,977).

B. hWART2 Nucleic Acid

The full-length human Wart2 cDNA is 5,276 bp long and consists of a 3,264 bp open reading frame (ORF) flanked by 394 and 1,612 bp of 5' and 3' untranslated regions (UTR) respectively. A 23 nucleotide polyA-rich tail follows the 3' UTR. This ORF has the potential to encode a 1,088 amino acid polypeptide. Based on amino acid sequence homology to the Drosophila and human Wart1 proteins we believe that this ORF encodes the human Wart2 protein. There are 5 additional ORF's, none longer than 144 nucleotides, 5' to nucleotide 375. The ATG at position 375 fits the Kozak consensus for translational initiation.

Fourteen EST and one STS fragment match the Wart2_h cDNA sequence. These ESTs cluster into 5 contigs and match the Wart2_h coding region at the following positions: N56660 at 712, R75698 at 3,077, H26525 at 3,109, R01798 at

2,751, AA30618 at 163. The latter is a TIGR EST whose 3' end matches position 5,276 at the 3' end of the Wart2 gene.

II. The Proteins of the Invention.

The open reading frame (ORF) of the full-length hWART1 nucleic acid molecule is predicted to encode a protein of 1130 amino acids with a predicted molecular weight of approximately 127 kDa. The ORF of the full-length hWART2 nucleic acid molecule is predicted to encode a protein of 1088 amino acids with a molecular weight of approximately 120 kDa. Structural analysis of these protein sequences predicts that hWART1 and hWART2 are likely to be intracellular proteins.

A. hWART1 Protein

Analysis of the deduced amino acid sequence predicts hWART1 to be an intracellular protein, lacking both a signal sequence and transmembrane domain. The predicted amino acid sequence contains a long N-terminal region that is believed to be predominately alpha helical and hydrophilic followed by a C-terminal domain with all the motifs characteristic of a serine-threonine kinase. Several regions of homology exist between the hWART1, hWART2 and *Drosophila* homologue. A Smith-Waterman pairwise alignment of hWART1 and hWART2 is shown in Fig. 1, and a similar alignment between hWART1 and *Drosophila* WART (SEQ ID NO:13) is shown in Fig. 2. The description and

boundaries of these motifs are described in the following paragraphs.

The extreme N-terminal region of the hWART1 protein extending from 12-45 amino acids, shares 66% identity and 78% similarity to the corresponding region in hWART2. This domain is referred to as "BOX A". Box B lies ten amino acids C-terminal to Box A and extends from amino acids 55-151. Box B shares 56% identity and 77% similarity to the corresponding region in hWART2. *Drosophila* WART protein lacks significant homology to the N-terminal Box A and B present in the two human proteins. A Smith-Waterman search of the nonredundant protein database with the amino acid sequences of Box A and Box B does not reveal any significant homologies that might suggest a potential function for these two conserved regions.

hWART1 contains a proline-rich region, consisting of 26% prolines, extending from amino acids 236-377. This region is distantly similar to *Volvox* extensin proteins (40% amino acid identity with *Volvox cateri* extensin GB:x65165 using Smith-Waterman alignment) and may represent a protein interaction domain as well as a possible site for interaction with proteins containing SH3 motifs. WART homologues from *Drosophila melanogaster* (PIR:A56155) and *Caenorhabditis elegans* (EMBL:Z8159) have an N-terminal proline-rich comparable to the one found in hWART1, but this region is lacking in hWART2. Box C extends from amino acids 404-520 and is 44% identical and 73% similar to

hWART2. A small portion of Box C is also found in a similar position in *D. melanogaster* WART but is mostly replaced with a glutamine-rich region. A Smith-Waterman search of the nonredundant protein database with the amino acid sequence of Box C did not reveal significant homologies that would suggest a potential function for this region. The 5' amino acid motif P₄Y is present between amino acids 555-559 of hWART1 and is conserved in hWART2 and *Drosophila* WART. This region may represent an SH3 or WW domain binding site or may be a site for tyrosine phosphorylation and SH2 interactions.

A distinguishing feature of the WART family is the extended homology flanking both the N- and C-terminal side of their predicted serine-threonine kinase domain. This extended homology is present in the human and mouse WART1 and WART2, *D. melanogaster* WART, and *C. elegans* WART. The N-terminal flanking region of the hWART1 catalytic domain extends from amino acids 601-702 of hWART1 and is 69%, 71%, and 45% identical and 85%, 85%, and 64% similar with hWART2, *D. melanogaster* WART, and *C. elegans* WART, respectively. The catalytic domain of WART1 (amino acids 691-998) is 85%, 75%, and 53% identical 90%, 87%, and 72% similar with hWART2, *D. melanogaster* WART, *C. elegans* WART, respectively. The region C-terminal to the catalytic domain, extending from amino acids 1011-1086 in hWART1 is 63%, 53%, and 40% identical and 76%, 73%, and 56% similar

with hWART2, *D. melanogaster* WART, and *C. elegans* WART, respectively.

The extended homology on either side of the catalytic domain of the WART kinases suggests these regions may actually be a part of this enzymatic domain. Other Serine-threonine kinases including Calmodulin-dependent kinases and DUN1 kinases from *S. cerevisiae*, are also characterized by an extended kinase domain.

B. hWART2 Protein

The 5276 bp human WART2 sequence is predicted to encode a polypeptide of 1,088 amino acids (SEQ ID NO:4). Analysis of the deduced amino acid sequence predicts hWART2 to be an intracellular protein, lacking both a signal sequence and transmembrane domain. Like hWART1, it contains a long N-terminal region that is predominately alpha helical and hydrophilic followed by a C-terminal domain with all the motifs characteristic of a serine-threonine kinase. Several regions of homology exist between hWART1, hWART2 and the *Drosophila* homologue (Figs. 1 and 2). Box A extends from amino acids 1-33 and is 66% identical and 78% similar to the corresponding region in hWART1. Box B lies 21 amino acids C-terminal to Box A from amino acids 43-139. The hWART2 Box B is 56% identical and 77% similar to the corresponding region in hWART1. Box C extends from amino acids 342-466 and is 44% identical and 73% similar to hWART1. A GC nucleotide repeat region

encodes alternating prolines and alanines (PAPA Box) from amino acids 467-480. This motif is also present in the human Cdk-inhibitor p57KIP2 (GB:U22398), and in the myosin light chain protein from several species. A recent study examined the human p57KIP2 for genetic variations in a large number of tumors (Tokino et al., "Characterization of the human p57 (KIP2) gene: alternative splicing, insertion/deletion polymorphisms in VNTR sequences in the coding region, and mutational analysis." Hum. Genet. 97:625-631, 1996). This study identified 4 types of 12-bp deletions in the proline/alanine rich region of p57KIP2, none of which were somatic mutations, suggesting that the GC repeat region of hWART2 may also be subject to variations in size, possibly resulting in altered gene function. The P₄Y motif lies at amino acids 514-518 in hWART2 and is also found in a similar location in hWART1 and *D. melanogaster* WART.

The region immediately N-terminal to the core of the WART2 kinase domain extends from amino acid 564-665 and is 69%, 65%, and 41% identical and 85%, 82%, and 62% similar with human WART1, *D. melanogaster* WART, and *C. elegans* WART, respectively. The catalytic domain of WART2 (amino acids 666-973) is 85%, 75%, and 53% identical and 90%, 86%, and 70% similar with hWART1, *D. melanogaster* WART, and *C. elegans* WART, respectively. The region C-terminal to the catalytic domain extends from amino acids 974-1048 in WART2 is 63%, 50%, and 36% identical and 76%, 72%, and 60%

similar with hWART1, *D. melanogaster* WART, and *C. elegans* WART1, respectively.

III. Applications, Biological Significance, and Clinical Utility of hWARTs

Experimental studies of the WART homologues from lower organisms suggest hWART1 may play a role in the regulation of normal epithelial cell growth. Therefore, compounds that specifically modulate the function of these proteins would likely alter the growth or biology of epithelial tumors and would provide novel potential treatments for human cancer.

IV. A Nucleic Acid Probe for the Detection of hWARTs

A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain another nucleic acid molecule of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (e.g. "Molecular Cloning: A Laboratory Manual", second edition, edited by Sambrook, Fritsch, & Maniatis, Cold Spring Harbor Laboratory, 1989).

In the alternative, chemical synthesis is carried out in order to obtain nucleic acid probes having nucleotide sequences which correspond to N-terminal and C-terminal portions of the amino acid sequence of the polypeptide of

interest. Thus, the synthesized nucleic acid probes may be used as primers in a polymerase chain reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "PCR Protocols, A Guide to Methods and Applications", edited by Innis et al., Academic Press, 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art (e.g. "Molecular Cloning: A Laboratory Manual", second edition, edited by Sambrook, Fritsch, & Maniatis, Cold Spring Harbor Laboratory, 1989). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA as well as DNA probes and nucleic acids modified in the sugar, phosphate or even the base portion as long as the probe still retains the ability to specifically hybridize under conditions as disclosed herein. Such probes are generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include,

but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins, such as polyacrylamide and latex beads, and nitrocellulose. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The sample used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed.

Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample which is compatible with the method utilized.

V. A Probe Based Method And Kit For Detecting hWART

One method of detecting the presence of hWART in a sample comprises (a) contacting the sample with one of the above-described nucleic acid probes, under conditions such that hybridization occurs, and (b) detecting the presence of the probe bound to a nucleic acid molecule in the sample. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of hWART in a sample comprises at least one container having disposed therein an above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to radiolabelled probes, enzymatically labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or streptavidin).

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention

can readily be incorporated into one of the established kit formats which are well known in the art.

VI. DNA Constructs Comprising an hWART Nucleic Acid Molecule and Cells Containing These Constructs

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and one of the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and a nucleic acid molecule described herein. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complimentary to an RNA sequence encoding an amino acid sequence corresponding to an hWART polypeptide, or functional derivative, and a transcriptional termination region functional in said cell.

The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an hWART nucleic acid molecule, as described herein, and thereby is capable of expressing a peptide. The polypeptide may be purified from cells which have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the regulatory regions needed for gene sequence expression may vary from organism to organism, but will in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding an hWART gene may be obtained by the above-described cloning methods. This region may be

retained for its transcriptional termination regulatory sequences, such as termination and polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding an hWART gene, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and an hWART sequence) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of the second sequence, for example an hWART gene sequence, or (3) interfere with the ability of the second sequence to be transcribed by the promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence. Thus, transcriptional and translational signals recognized by an appropriate host are necessary to express an hWART gene.

The present invention encompasses the expression of an hWART gene (or a functional derivative thereof) in either prokaryotic or eukaryotic cells. Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of

preferred expression system for these genes. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include λ gt10, λ gt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

Recognized prokaryotic hosts include bacteria such as *E. coli* and those from genera such as *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

To express hWART (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the gene sequence to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (i.e., inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage λ , the *bla* promoter of the β -lactamase gene

sequence of pBR322, and the CAT promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage λ (P_L and P_R), the trp, recA, lacZ, lacI, and gal promoters of *E. coli*, the α -amylase (Ulmanen, et al., *J. Bacteriol.* 162:176-182, 1985) and the sigma-28-specific promoters of *B. subtilis* (Gilman, et al., *Gene* 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: *The Molecular Biology of the Bacilli*, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward, et al., *Mol. Gen. Genet.* 203:468-478, 1986). Prokaryotic promoters are reviewed by Glick, *J. Ind. Microbiol.* 1:277-282, 1987; Cenatiempo, *Biochimie* 68:505-516, 1986; and Gottesman, *Ann. Rev. Genet.* 18:415-442, 1984.

Proper expression in a prokaryotic cell also requires the presence of a ribosome binding site upstream of the gene sequence-encoding sequence. Such ribosome binding sites are disclosed (see, for example, Gold, et al., *Ann. Rev. Microbiol.* 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene.

As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include the progeny of the cells. Thus, the words "transformants" or "transformed cells" include the

primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations.

However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the hWART peptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, and mammalian cells, either *in vivo* or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO, 3T3 or CHO-K1, or cells of lymphoid origin (such as 32D cells) and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332 and PC12 which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase

promoter can be used (Rubin, Science 240:1453-1459, 1988).

Alternatively, baculovirus vectors can be engineered to express large amounts of hWART in insects cells (Jasny, Science 238:1653, 1987; Miller, et al., In: Genetic Engineering, 1986; Setlow, J.K., et al., eds., Plenum, Vol. 8, pp. 277-297).

Any of a series of yeast gene sequence expression systems can be utilized which incorporate promoter and termination elements from the actively expressed gene sequences coding for glycolytic enzymes; the systems are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational peptide modifications. A number of recombinant DNA strategies exist which utilize strong promoter sequences and high copy number of plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian gene sequence products and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). For a mammalian host, several possible vector systems are available for the expression of hWART.

A particularly preferred yeast expression system is that utilizing *Schizosaccharomyces pombe*. This system is useful for studying the activity of members of the Src family (Superti-Furga, et al., EMBO J. 12:2625, 1993) and

other non-receptor-TKs, the function of which is often regulated by the activity of tyrosine phosphatases.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of hWART in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer, et al., J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early

promoter (Benoist, et al., Nature (London) 290:304-310, 1981); and the yeast gal4 gene sequence promoter (Johnston, et al., Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver, et al., Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon which encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes hWART (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (i.e., AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as an hWART coding sequence).

An hWART nucleic acid molecule and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA (or RNA) molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule (a plasmid). Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent or stable expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of single chain binding protein mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama, *Mol. Cell. Bio.* 3:280, 1983.

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector; the number of copies of the vector which are desired in a

particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColE1, pSC101, pACYC 184, pVX). Such plasmids are, for example, disclosed by Sambrook (*c.f.* "Molecular Cloning: A Laboratory Manual", second edition, edited by Sambrook, Fritsch, & Maniatis, Cold Spring Harbor Laboratory, 1989). *Bacillus* plasmids include pC194, pC221, pT127, and the like. Such plasmids are disclosed by Gryczan (In: *The Molecular Biology of the Bacilli*, Academic Press, NY, 1982, pp. 307-329). Suitable *Streptomyces* plasmids include p1J101 (Kendall, et al., *J. Bacteriol.* 169:4177-4183, 1987), and *streptomyces* bacteriophages such as fC31 (Chater, et al., In: *Sixth International Symposium on Actinomycetales Biology*, Akademiai Kiado, Budapest, Hungary, 1986, pp. 45-54). *Pseudomonas* plasmids are reviewed by John, et al., *Rev. Infect. Dis.* 8:693-704, 1986, and Izaki, *Jpn. J. Bacteriol.* 33:729-742, 1978.

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein, et al., *Miami Wntr. Symp.* 19:265-274, 1982); Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470 1981;

Broach, Cell 28:203-204, 1982; Bollon et al., J. Clin. Hematol. Oncol. 10:39-48, 1980; Maniatis, In: Cell Biology: A Comprehensive Treatise, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980.

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, i.e., transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene molecule(s) results in the production of hWART or fragments or functional derivatives thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions for the transformed cells can be used to foster expression of the polypeptides of the present invention. The most preferred conditions are those which mimic physiological conditions.

VII. An Antibody Having Binding Affinity to an hWART
Polypeptide and Hybridomas Producing The Antibody

The present invention also relates to an antibody having specific binding affinity to an hWART polypeptide. The polypeptide may have the amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4, or a fragment thereof, or at least 41 contiguous amino acids thereof. Such an antibody may be identified by comparing its binding affinity to the desired polypeptide, for example an hWART polypeptide, with its binding affinity to another (non-hWART) polypeptide. Those which bind selectively to the desired polypeptide would be chosen for use in methods requiring a distinction between the desired polypeptide and other polypeptides. Such methods could include, but should not be limited to, the analysis of altered expression of the desired polypeptide in tissue containing other polypeptides and assay systems using whole cells.

An hWART polypeptide of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide would be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting. The present

invention also relates to a hybridoma which produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth et al., J. Immunol. Methods 35:1-21, 1980). Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal which is immunized, the antigenicity of the polypeptide and the site of injection.

The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or β -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Agl4 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz, et al., Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", supra, 1984).

For polyclonal antibodies, antibody containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, see (Stemberger, et al., J. Histochem. Cytochem.

18:315, 1970; Bayer, et al., Meth. Enzym. 62:308, 1979; Engval, et al., Immunot. 109:129, 1972; Goding, J. Immunol. Meth. 13:215, 1976). The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues which express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir et al., "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby, et al., Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as in immunochromotography.

Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed above with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed anti-peptide peptides, for example see Hurby et al., "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp.

289-307, 1992, and Kaspczak, et al., Biochemistry
28:9230-8, 1989.

VIII. An Antibody Based Method And Kit For Detecting
hWART

The present invention encompasses a method of detecting an hWART polypeptide in a sample comprising incubating a test sample with one or more of the antibodies of the present invention and determining whether the antibody binds to the test sample. The method can include the steps of, for example: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. Altered levels, either an increase or decrease, of hWART in a sample as compared to normal levels may indicate an abnormality or disorder.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be

found in Chard, "An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands 1986; Bullock et al., "Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, "Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands (1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily adapted in order to obtain a sample which is compatible with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container containing an above-described antibody, and (ii) a second container containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and

reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats which are well known in the art.

IX. Isolation of Natural Binding Partners of hWART

The present invention also relates to methods of detecting natural binding partners capable of binding to an hWART polypeptide. A natural binding partner of hWART may be, for example, a substrate protein which is dephosphorylated as part of a signaling cascade. The binding partner(s) may be present within a complex mixture, for example, serum, body fluids, or cell extracts.

In general, methods for identifying natural binding partners comprise incubating a substance with a first polypeptide, hWART for the invention described herein, and detecting the presence of a substance bound to the first polypeptide. Preferred methods include the two-hybrid system of Fields and Song (supra) and

co-immunoprecipitation wherein the first polypeptide is allowed to bind to a natural binding partner, then the polypeptide complex is immunoprecipitated using antibodies specific for the first polypeptide. The natural binding partner can then be isolated and identified by techniques well known in the art.

X. Identification of and Uses for Substances Capable of Modulating hWART Activity

The present invention also relates to a method of detecting a substance capable of modulating hWART activity.

Such substances can either enhance activity (agonists) or inhibit activity (antagonists). Agonists and antagonists can be peptides, antibodies, products from natural sources such as fungal or plant extracts or small molecular weight organic compounds. In general, small molecular weight organic compounds are preferred. Examples of classes of compounds that can be tested for hWART modulating activity are, for example but not limited to, thiazoles (see, for example US applications 60/033,522 filed December 19, 1996, and 08/660,900 filed June 7, 1996), and naphthopyrones (US patent number 5,602,171, issued February 11, 1997).

In general the method comprises incubating cells that produce hWART in the presence of a test substance and detecting changes in the level of hWART activity or hWART binding partner activity. A change in activity may be manifested by increased or decreased binding of an hWART

polypeptide to a natural binding partner or increased or decreased biological response in cells. Biological responses can include, for example, proliferation, differentiation, survival, or motility. The substance thus identified would produce a change in activity indicative of the agonist or antagonist nature of the substance. Once the substance is identified it can be isolated using techniques well known in the art, if not already available in a purified form.

The present invention also encompasses a method of agonizing (stimulating) or antagonizing hWART associated activity in a mammal comprising administering to said mammal an agonist or antagonist to hWART in an amount sufficient to effect said agonism or antagonism. Also encompassed in the present application is a method of treating diseases in a mammal with an agonist or antagonist of hWART-related activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize hWART associated function(s). The particular compound can be administered to a patient either by itself or in a pharmaceutical composition where it is mixed with suitable carriers or excipient(s). In treating a patient, a therapeutically effective dose of the compound is administered. A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient.

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals. Cell culture assays and animal studies can be used for determining the LD_{50} (the dose lethal to 50% of a population) and the ED_{50} (the dose therapeutically effective in 50% of a population). The dose ratio between toxic and therapeutic effects is the therapeutic index, which can be expressed as the ratio LD_{50}/ED_{50} . Compounds which exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosages for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized.

For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays by determining an IC_{50} (i.e., the concentration of the test compound which achieves a half-maximal disruption of the protein complex, or a half-maximal inhibition of the cellular level and/or activity of a cellular component, ex. hWART). A dose can then be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} as determined in cell culture. Such information can be

used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by HPLC. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., in "The Pharmacological Basis of Therapeutics", Ch. 1 p1, 1975).

It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions.

Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administered dose in the management of the oncogenic disorder of interest will vary with the severity of the condition to be treated and to the route of administration.

The severity of the condition may, for example, be evaluated, in part, by standard prognostic evaluation methods. Further, the dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above may be used in veterinary medicine.

Depending on the specific conditions being treated, such agents may be formulated and administered systemically or locally. Techniques for formulation and administration may be found in "Remington's Pharmaceutical Sciences," 1990, 18th ed., Mack Publishing Co., Easton, PA. Suitable routes may include oral, rectal, transdermal, vaginal,

transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections, just to name a few.

For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular those formulated as solutions, may be administered parenterally, such as by intravenous injection. The compounds can be formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral

ingestion by a patient to be treated. Particular formulations suitable for parenteral administration of hydrophobic compounds can be found in US Patent No. 5,610,173, issued March 11, 1997 and US Provisional Application Serial No. 60/039,870, filed March 05, 1997, both of which are hereby incorporated by reference herein in their entirety, including any figures and drawings.

Agents intended to be administered intracellularly may be administered using techniques well known to those of ordinary skill in the art. For example, such agents may be encapsulated into liposomes, then administered as described above. Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external microenvironment and, because liposomes fuse with cell membranes, are efficiently delivered into the cell cytoplasm. Small organic molecules may be directly administered intracellularly due to their hydrophobicity.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an amount effective to achieve its intended purpose. Determination of an effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated for oral administration may be in the form of tablets, dragees, capsules, or solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores.

Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethylcellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as

glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers.

In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

The present invention also includes a kit containing the the active ingredients mentioned above. The kit may or may not include other compounds, such as carriers or excipients, and the active ingredient may be included in a suitable pharmaceutical composition. The kit may include a protocol for the use of the compounds of the invention. Said protocol may be approved by the Food and Drug Administration or an equivalent agency.

XI. Transgenic Animals

Also contemplated by the invention are transgenic animals useful for the study of hWART activity in complex *in vivo* systems. A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode a human hWART polypeptide. Native expression in an animal may alternatively be reduced by providing an amount of antisense RNA or DNA effective to reduce expression of the target gene.

A variety of methods are available for the production of transgenic animals associated with this invention. DNA sequences encoding hWART can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (e.g., the nucleus of a two-cell embryo) following the initiation of cell division (Brinster, et al., Proc. Nat. Acad. Sci. USA 82: 4438, 1985). Embryos can be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from

such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term.

Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan, et al., supra). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout, *Experientia* 47: 897-905, 1991. Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sandford et al., July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. After being allowed to mate, the females are sacrificed by CO₂ asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice. See Hammer, et al., *Cell* 63:1099-1112, 1990.

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art. (See, for example, Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987). In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, a gene encoding neomycin resistance is physically linked to the sequence(s) of the invention. Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination. (See Capecchi, *Science* 244: 1288, 1989.) Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner et al., *Nature* 338: 153, 1989, the teachings of which are incorporated by reference herein. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the

blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others. (See Houdebine and Chourrout, *supra*; Pursel, et al., *Science* 244:1281, 1989; Simms, et al., *Bio/Technology* 6:179, 1988.)

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding an hWART polypeptide or a gene effecting the expression of an hWART polypeptide. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introducing an hWART polypeptide, or for regulating the expression of an hWART polypeptide (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

XIII. Gene Therapy

hWART nucleic acid sequences, both mutated and non-mutated, will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated positive initial results. The basic science of gene therapy is described in Mulligan, Science 260:926, 1993. As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In one preferred embodiment, an expression vector containing an hWART coding sequence or an hWART mutant coding sequence, as described above, is inserted into cells, the cells are grown *in vitro* and then infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous hWART in such a manner that the promoter segment enhances expression of the endogenous hWART gene (for example, the promoter segment is

transferred to the cell such that it becomes directly linked to the endogenous hWART gene).

The gene therapy may involve the use of an adenovirus containing hWART cDNA targeted to an appropriate cell type, systemic hWART increase by implantation of engineered cells, injection with hWART virus, or injection of naked hWART DNA into appropriate cells or tissues, for example adipose tissue.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, other RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (eg., cDNA) encoding recombinant hWART protein into the targeted cell population (e.g., tumor cells or fat cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences. See, for example, the techniques described in Maniatis et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, N.Y. (1989), and in Ausubel et al., *Current Protocols in Molecular Biology*, Greene Publishing Associates and Wiley Interscience, N.Y. (1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in reconstituted system eg., liposomes or other lipid systems for delivery to target cells (See eg., Felgner et al., *Nature* 337:387-8, 1989). Several other methods for the direct transfer of plasmid DNA into

cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins. See, Miller, *supra*.

In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection. (Capecchi MR, *Cell* 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is precipitated with CaPO₄ and taken into cells by pinocytosis (Chen C. and Okayama H, *Mol. Cell Biol.* 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu G., et al., *Nucleic Acids Res.*, 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner PL., et al., *Proc. Natl. Acad. Sci. USA.* 84:7413-7, 1987); and particle bombardment using DNA bound to small projectiles (Yang NS., et al., *Proc. Natl. Acad. Sci.* 87:9568-72, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake

of DNA into cells. The admixture of adenovirus to solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene. (Curiel, et al., Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic acid molecule into a cell. Gene transfer is commonly performed to enable the expression of a particular product encoded by the gene. The product may include a protein, polypeptide, antisense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

In another preferred embodiment, a vector having nucleic acid sequences encoding an hWART is provided in which the nucleic acid sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression as set forth in International Publication No. WO

93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, an hWART nucleic acid is used in gene replacement. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene which is missing or defective in the animal. Methods of introducing the nucleic acid into the animal to be treated are as described above.

One skilled in the art appreciates that any modifications made to a complex can be manifested in a modification of any of the molecules in that complex. Thus, the invention includes any modifications to nucleic acid molecules, polypeptides, antibodies, or compounds in a complex. All of these aspects and features are explained in detail with respect to PYK-2 in PCT publication WO 96/18738, which is incorporated herein by reference in its entirety, including any drawings. Those skilled in the art will readily appreciate that such descriptions can be easily adapted to hWART polypeptides and nucleic acid

molecules as well, and is therefore equally applicable to the present invention.

XIII. Compounds that Modulate the Function of hWART Proteins

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire et al.), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari et al.), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny et al.), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow et al.). The compounds that can traverse cell membranes and are resistant to acid

hydrolysis are potentially advantageous therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976, published August 1, 1996 by Ballinari et al. describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang et al. (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang et al. (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari et al., all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as

monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang et al. (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang et al. (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari et al. teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating hWART activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines.

The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazoline include Barker et al., EPO Publication No. 0 520 722 A1; Jones et al., U.S. Patent No. 4,447,608; Kabbe et al., U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker et al., Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research

9(2 part 1):293-304 (1979); Curtin et al., Br. J. Cancer 53:361-368 (1986); Fernandes et al., Cancer Research 43:1117-1123 (1983); Ferris et al. J. Org. Chem. 44(2):173-178; Fry et al., Science 265:1093-1095 (1994); Jackman et al., Cancer Research 51:5579-5586 (1981); Jones et al. J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus et al., J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell et al., Magnetic Resonance in Medicine 17:189-196 (1991); Mini et al., Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece et al., Cancer Research 47(11):2996-2999 (1977); Sculier et al., Cancer Immunol. and Immunother. 23:A65 (1986); Sikora et al., Cancer Letters 23:289-295 (1984); Sikora et al., Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle et al., J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke et al., J. Med. Chem. 36:425-432 (1993); and Burke et al. BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., " J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S.

patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

EXAMPLES

The examples below are non-limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of novel human WART nucleic acids and polypeptides.

EXAMPLE 1: Cloning of Murine WART1

Total RNAs were isolated using the Guanidine Salts/Phenol extraction protocol of Chomczynski and Sacchi (P. Chomczynski and N. Sacchi, Anal. Biochem. 162:156, 1987) from murine embryos from gestational day 12. These RNA were used to generate single-stranded cDNA using the Superscript Preamplification System (GIBCO BRL, Gaithersburg, MD; Gerard, GF et al., Focus 11:66, 1989). A typical reaction used 10 µg total RNA with 1.5 µg oligo(dT)₁₂₋₁₈ in a reaction volume of 60 µl. The product was treated with RNaseH and diluted to 100 µl with H₂O. For subsequent PCR amplification, 1-4 µl of the sscDNA was used in each reaction.

Degenerate oligonucleotides targeted for the Epidermal Growth Factor (EGF) family were synthesized on an Applied Biosystems 3948 DNA synthesizer using established

phosphoramidite chemistry, precipitated with ethanol and used unpurified for PCR. The sequence of the degenerate oligonucleotide primers used were the following:

KITDFG = 5' - CAYGTNAARATHACNGAYTTYGG - 3' (SEQ ID NO:5) and

KCWMID = 5' - GGRTCDATCATCCAGCAYTT- 3' (SEQ ID NO:6).

These primers were derived from the sense and antisense strands, respectively of peptide sequences KITDFG (SEQ ID NO:7) and KCWMID (SEQ ID NO:8).

Degenerate nucleotide residue designations are: N = A, C, G, or T; R = A or G; Y = C or T; H = A, C or T not G; and D = A, G or T not C.

PCR reactions were performed using degenerate primers applied to the murine day 12 embryo single-stranded cDNA. The primers were added at a final concentration of 5 μ M each to a mixture containing 10 mM TrisHCL (pH 8.3), 50 mM KCL, 1.5 mM MgCl₂, 200 μ M each deoxynucleoside triphosphate, 0.001% geletin, 1.5 U AmpliTaq DNA Polymerase (Perkin-Elmer/Cetus), and 1-4 μ l cDNA. Following 3 min denaturation at 95°C, the cycling conditions were 94°C for 30 s, 50°C for 1 min, and 72°C for 1 min 45 s for 35 cycles.

PCR fragments migrating between 300-350 bp were isolated from 2% agarose gels using the GeneClean Kit (Bio101), and T-A cloned into the pCRII vector (Invitrogen Corp. U.S.A.) according to the manufacturer's protocol.

Colonies were selected for mini plasmid DNA-preparations using Qiagen columns and the plasmid DNA was

sequenced using cycle sequencing dye-terminator kit with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA).

Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer, and analyzed using the BLAST alignment algorithm (Altschul, S.F. et al., J.Mol.Biol. 215:403-10).

This analysis lead to the isolation of clone 105-4-10 corresponding to murine WART1.

Clone 105-4-10 exhibits 65% homology with the predicted amino acid sequence of the *Drosophila* serine-threonine kinase WART (Gene Bank (GB): L39847) using MPsrch_tnp (Oxford Molecular Group, UK) a DNA to protein pairwise search implementation of the Smith-Waterman algorithm. While the 5' primer recognized a sequence encoding the predicted kinase homology domain, the 3' primer hybridized to a sequence whose translation was out of frame with the peptide it had been designed to amplify.

Nonetheless, the intervening sequence contained the expected kinase motifs.

EXAMPLE 2: cDNA Cloning and Characterization of Human WART1

A second PCR strategy was designed to isolate the human orthologue of the novel mouse clone. Degenerate primers based on clone 105-4-10 were used to amplify templates derived from a pool of primary human non-small cell lung carcinomas. Total RNAs from primary human lung

tumors were isolated as in Example 1. The sequence of the degenerate oligonucleotide primers used were as follows:

5774 = 5'- TCCRAACAGDATNACNCCNACNSWCCA - 3' (SEQ ID NO:9)

and

5326 = 5' - TTYGGNYTNTGYACNGGNTTYMGNTGG - 3' (SEQ ID NO:10).

These primers were derived from the sense and antisense strands, respectively of peptide sequences FGLCTGFRW (SEQ ID NO:11) and WSVGVLFE (SEQ ID NO:12) present in the murine WART1 clone. The amplification conditions were similar to those described in Example 1 using oligonucleotides KITDFG (SEQ ID NO:7 and KCWMID (SEQ ID NO:8). Two distinct PCR products were isolated, SuSTK15 (268 bp) and SuSTK17 (273 bp). These two fragments share 72% DNA identity and 88% amino acid sequence identity to one another. SuSTK15_h has been designated as hWART1 cDNA because it is more related to the murine WART1 cDNA (90% DNA identity; 98% amino acid identity), than SuSTK17_h (74% DNA sequence identity; 83% amino acid identity). SuSTK17_h has been designated as hWART2.

EXAMPLE 3: Isolation of hWART1

A human bone marrow λ gt11 cDNA library was probed with the PCR fragments corresponding to human WART1. Probes were 32 P-labeled by random priming and used at 2×10^6 cpm/ml following standard techniques known in the art for library screening. Prehybridization (3h) and hybridization

(overnight) were conducted at 42°C in 5xSSC, 5x Denhart's solution, 2.5% dextran sulfate, 50 mM Na₂PO₄ [pH 7.0], 50% formamide with 100 mg/ml denatured salmon sperm DNA. Stringent washes were performed at 65°C in 0.1x SSC and 0.1% SDS. DNA sequencing was carried out on both strains using a cycle sequencing dye-terminator kit with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Three cDNAs were isolated and completely sequenced. Two of the clones were found to be overlapping clones that encoded a long C-terminal open reading frame (ORF) but lacked an upstream stop codon. The third clone was found to contain no significant ORFs but was later found to encode the 3' untranslated region (UTR) of the human WART1 cDNA. Rescreening of the bone marrow cDNA library yielded two more cDNA clones which upon sequencing were found to contain a long ORF contiguous with the two clones isolated from the previous screening of the bone marrow cDNA library.

The full-length human WART1 cDNA is 7,382 bp long and consists of a 3,390 bp ORF. This ORF is flanked by 394 and 3,554 bp of 5' and 3' untranslated regions (UTR) respectively. A 41 nucleotide polyA-rich tail follows the 3' UTR. There are two potential start codons at positions 395 and 431, neither corresponding to the Kozak consensus for initiating methionines. Although the second start site

aligns to the N-terminal sequence of the related WART2, we have designated position 395 as the start site since it is the first start site encountered in this extended ORF. There are two additional ATGs located 5' to the start codon at position 395, but they are followed by stop codons after 31 and 10 nucleotides, respectively. The 3,390 bp ORF has the potential to encode a 1,130 amino acid protein.

The 5' UTR from nucleotide 12-63 displays 10 copies of the tri-nucleotide repeat, GGC. This repeat is very similar to one found in the human retinoid X receptor beta (GB:M84820). Such repeats have been reported to undergo expansion in various human diseases particularly those associated with neuronal phenotypes. The 3' UTR contains an inverted 289 bp Alu-J subfamily repeat (between nucleotides 6,058-6,346). A polyadenylation signal (AATAAA) is found at position 7,338 followed by a 20 nucleotide long polyadenylated stretch.

Sequence analysis of multiple cDNA clones identified three polymorphisms in the human WART1 gene: (1) at nucleotide 978 resulting in an Ala/Gly change; (2) at nucleotide 1,840, silent; (3) at nucleotides 3,252-3,253 comprising a deletion of two adenosines that results in a C-terminal truncation of the hWART1 gene, disrupting the putative kinase domain. The frame shift mutation at position 3252 was observed in two independent clones isolated from the human bone marrow cDNA source. The non-mutated sequence, however, was also confirmed in multiple

independent clones. Conceivably, truncation of the WART1 Serine-threonine kinase could play a role in disease progression.

EXAMPLE 4: Isolation of cDNA Encoding the hWART2 Gene

SuSTK17_h was used as a probe to screen a λ gt11 human bone marrow cDNA library. Multiple cDNA clones were isolated and two (W2D4 and W2D1.8) were sequenced fully on both strands. Clone W2D4 lies 5' of clone W2D1.8 separated by an internal *EcoRI* site in the full-length hWART2 cDNA.

The full-length 5,276 bp hWART2 cDNA consists of a 3,264 bp ORF flanked by 394 and 1,612 bp of 5' and 3' UTRs, respectively. A 23 nucleotide polyA-rich tail follows the 3' UTR. This ORF has the potential to encode a 1,088 amino acid polypeptide. Based on amino acid sequence homology to the *Drosophila* and human WART1 proteins we believe that this ORF encodes the hWART2 protein. There are 5 additional ORF's none longer than 144 nucleotides, 5' to nucleotide 375. The ATG at position 375 fits the Kozak consensus for translational initiation.

EXAMPLE 5: Distribution of Human WART1 and WART2 mRNA in Normal Tissues and Tumor Cell Lines:

Northern blots were obtained from Clontech (Palo Alto, CA) containing 2 μ g polyA+ RNA from 16 different adult human tissues (spleen, thymus, prostate, testis, ovary, small intestine, colonic mucosa, heart, brain, placenta,

lung, liver, skeletal muscle, kidney, pancreas, and peripheral blood leukocytes), and four different human fetal tissues (brain, lung, liver, and kidney), on charge-modified nylon membrane. Additional Northern blots were prepared by running 20 µg total RNA on formaldehyde 1.2% agarose gel and transferring to nylon membranes.

Filters were hybridized with random prime [³²P]dCTP-labeled probes synthesized from the 270 bp inserts from SuSTK15 (hWART1) or SuSTK17 (hWART2). Hybridization was performed at 60°C overnight in 6XSSC, 0.1% SDS, 1X Denhardt's solution, 100 mg/ml denatured herring sperm DNA with 1-2 x 10⁶ cpm/ml of ³²P-labeled DNA probes. The filters were washed in 0.1XSSC/0.1% SDS, 65°C, and exposed overnight on Kodak XAR-2 film.

hWART1 RNA expression was not detected in 18 normal samples tested. Similarly hWART2 expression was undetectable in 15 of the 18 samples, but was seen in three hormonally responsive tissues: uterus, prostate, and testis.

Expression of hWART1 and hWART2 was next examined in a panel of human tumor cell lines representing a diverse sampling of tumor types. hWART1 showed strong expression in cell lines from non-small cell lung cancer, ovarian tumors, central nervous system tumors, renal tumors, and breast tumors. hWART2 expression was consistently expressed, although usually at lower levels than hWART1 in virtually all samples tested, except for most of the colon

cancer lines. The robust overexpression of hWART1 and hWART2 in tumor cells versus normal tissues may provide an attractive target for oncology drug development. The tissue distribution of hWART1 and hWART2 mRNA is summarized in Table 1.

Table 1: Expression of hWART1 and hWART2 in various tissues.

Cell type	Origin	hWART1* expression	hWART2* expression
Brain	Normal tissue	0	0
Cerebellum	Normal tissue	0	0
Thymus	Normal tissue	0	0
Salivary Gland	Normal tissue	0	0
Lung	Normal tissue	0	0
Heart	Normal tissue	0	0
Liver	Normal tissue	0	0
Pancreas	Normal tissue	0	0
Kidney	Normal tissue	0	0
Stomach	Normal tissue	0	0

Duodenum	Normal tissue	0	0
Uterus	Normal tissue	0	0
Prostate	Normal tissue	0	1
Skel. Muscle	Normal tissue	0	0
Placenta	Normal tissue	0	0
Fetal Brain	Normal tissue	0	0
Mammary Gland	Normal tissue	0	0
Testis	Normal tissue	0	1
HOP-92	Lung tumor	1	1
EKVX	Lung tumor	2	1
NCI-H23	Lung tumor	4	1
NCI-H226	Lung tumor	3	1
NCI-H322M	Lung tumor	4	1
NCI-H460	Lung tumor	1	0
NCI-H522	Lung tumor	1	1
A549	Lung tumor	1	0
HOP-62	Lung tumor	1	0

OVCAR-3	Ovarian tumor	0	0
OVCAR-4	Ovarian tumor	1	1
OVCAR-5	Ovarian tumor	1	1
OVCAR-8	Ovarian tumor	1	1
IGROV1	Ovarian tumor	2	1
SK-OV-3	Ovarian tumor	4	1
SNB-19	CNS tumor	4	0
SNB-75	CNS tumor	1	1
U251	CNS tumor	2	1
SF-268	CNS tumor	3	3
SF-295	CNS tumor	1	1
SF-539	CNS tumor	3	1
CCRF-CEM	Leukemia	3	0
K-562	Leukemia	4	0
MOLT-4	Leukemia	1	0
HL-60	Leukemia	0	0
RPMI 8226	Leukemia	1	0
SR	Leukemia	1	1

DU-145	Prostate	1	1
PC-3	Prostate	1	0
HT-29	Colon tumor	0	0
HCC-2998	Colon tumor	0	0
HCT-116	Colon tumor	0	0
SW620	Colon tumor	0	0
Colo 205	Colon tumor	0	0
HTC15	Colon tumor	2	1
KM-12	Colon tumor	0	0
UO-31	Colon tumor	0	1
SN12C	Kidney tumor	0	3
A498	Kidney tumor	0	0
CaKil	Kidney tumor	2	2
RXF-393	Kidney tumor	2	1
ACHN	Kidney tumor	0	0
786-0	Kidney tumor	3	0
TK-10	Kidney tumor	3	4
LOX IMVI	Melanoma	3	2

Malme-3M	Melanoma	0	1
SK-MEL-2	Melanoma	1	1
SK-MEL-5	Melanoma	0	1
SK-MEL-28	Melanoma	1	1
UACC-62	Melanoma	4	1
UACC-257	Melanoma	1	1
M14	Melanoma	1	1
MCF-7	Breast tumor	3	1
MCF-7/ADR RES	Breast tumor	1	1
Hs578T	Breast tumor	1	1
MDA-MB-231	Breast tumor	0	1
MDA-MB-435	Breast tumor	0	0
MDA-N	Breast tumor	0	1
BT-549	Breast tumor	1	1
T47D	Breast tumor	4	1

* No expression is represented by 0 and maximal expression is represented by 4.

EXAMPLE 6: hWART1 and hWART2 Expression Vector
Construction

Full length expression constructs were generated for hWART1 and hWART2 from fully sequenced cDNA clones. These intact ORFs were inserted into pCDNAII (Invitrogen) or pRK5 for transient expression in mammalian cells. The hWART constructs were also tagged, by PCR mutagenesis, at their carboxy-terminal ends with the *Haemophilus influenza* hemagglutinin (HA) epitope YPYDVPDYAS (SEQ ID NO:14) (U.K. Pati, Gene 114:285-288, 1992).

An N-terminal myristolated form of both hWART1 and hWART2 were also generated by addition of a 5' amino tag to both proteins by PCR mediated mutagenesis using techniques known to those skilled in the art. These altered fragments were inserted into the same expression vectors. These expression constructs will allow targeting of the recombinant WART proteins to the membrane, potentially enhancing or deregulating their biologic effects.

Dominant negative forms of hWART1 and hWART2 can be constructed by a lysine to alanine substitution at the ATP-binding site in their kinase domains.

EXAMPLE 7: Generation of hWART1- and hWART2-specific
Immunoreagents

hWART1- and hWART2-specific immunoreagents were raised in rabbits against KLH-conjugated synthetic peptides specific to the two proteins. The peptides were conjugated to a cysteine added to the C-terminal end of each peptide, using techniques known to those skilled in the art. Amino

acid sequences of the peptide immunogens and their location within the human WART1 and WART2 sequences are:

hWART1:

ISKPSKEDQPSLPK (SEQ ID NO:15) (aa576-589) N-terminal to kinase domain.

DDQNTGSEIKNRDLVYV (SEQ ID NO:16) (aa1114-1130) C-terminus.

hWART2

PsgKNSRDEEKRESRI (SEQ ID NO:17) (aa579-594) N-terminal to kinase domain.

SDLVDQTEGCQPVYV (SEQ ID NO:18) (1074-1088) C-terminus.

SEQ ID NO:17 has 2 amino acid differences from the hWART2 sequence, due to only partial sequence information present at the time of its synthesis. These changes have no apparent effect on the specificity of the antisera generated using it as an immunogen.

EXAMPLE 8: Transient Expression of hWART1 and hWART2 Constructs in Mammalian Cells

The hWART1 and hWART2 expression plasmids (10 µg DNA/100 mm plate) containing the wild type or HA-tagged hWART1, wild type or HA-tagged hWART2 or the myristolated forms of hWART1 and hWART2 were introduced into COS and 293 cells with lipofectamine (Gibco BRL). After 72 hours, the cells were harvested in 0.5 ml solubilization buffer (20 mM Hepes pH 7.35, 150 mM NaCl, 10% glycerol, 1% Triton X-100, 1.5 mM MgCl₂, 1 mM EGTA, 2 mM phenylmethylsulfonyl fluoride, 1 µg/ml aprotinin). Sample aliquots were resolved by SDS polyacrylamide gel electrophoresis (PAGE) on 8% acrylamide/0.5% bis-acrylamide gels and electrophoretically transferred to nitrocellulose. Non-specific binding was blocked by preincubating blots in Blotto (phosphate buffered saline containing 5% w/v non-fat dried milk and 0.2% v/v nonidet P-40 (Sigma)), and recombinant protein was detected using a murine Mab to the HA decapeptide tag. Alternatively, recombinant protein can be detected using various hWART1- or hWART2- specific antisera.

Example 9: Screening Systems for the Identification of
Inhibitors of
hWART Activity

Assays may be performed in vitro or in vivo and are described in detail herein or can be obtained by modifying existing assays, such as the growth assay described in patent application Serial No. 08/487,088 (Lyon & Lyon Docket No. 212/276), filed June 7, 1995, by Tang et al., and entitled "Novel Pharmaceutical Compounds", or the assays described in patent application Serial No. 60/005,167 (Lyon & Lyon Docket No. 215/256), filed October 13, 1995 by Seedorf et al., and entitled "Diagnosis and Treatment of TKA-1 related disorders", all of which are hereby incorporated herein by reference in their entirety including any drawings. Another assay which could be modified to use the genes of the present invention is described in International Application No. WO 94/23039, published October 13, 1994, hereby incorporated herein by reference in its entirety including any drawings.. Other possibilities include detecting kinase activity in an autophosphorylation assay or testing for kinase activity on standard substrates such as histones, myelin basic protein, gamma tubulin, or centrosomal proteins. Binding partners may be identified by putting the N-terminal portion of the protein into a two-hybrid screen or detecting phosphotyrosine of a dual specificity kinase (Fields and Song, U.S. Patent No. 5,283,173, issued February 1, 1994, incorporated by reference herein, including any drawings).

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains. All patents and publications are herein incorporated by reference to the same extent as if each individual publication was specifically and individually indicated to be incorporated by reference.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance

herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

In view of the degeneracy of the genetic code, other combinations of nucleic acids also encode the claimed

peptides and proteins of the invention. For example, all four nucleic acid sequences GCT, GCC, GCA, and GCG encode the amino acid alanine. Therefore, if for an amino acid there exists an average of three codons, a polypeptide of 100 amino acids in length will, on average, be encoded by 3^{100} , or 5×10^{47} , nucleic acid sequences. It is understood by those skilled in the art that, with, Thus, a nucleic acid sequence can be modified to form a second nucleic acid sequence, encoding the same polypeptide as encoded by the first second nucleic acid sequences, using routine procedures and without undue experimentation. Thus, all possible nucleic acids that encode the claimed peptides and proteins are also fully described herein, as if all were written out in full taking into account the codon usage, especially that preferred in humans.

Furthermore, changes in the amino acid sequences of polypeptides, or in the corresponding nucleic acid sequence encoding such polypeptide, may be designed or selected to take place in an area of the sequence where the significant activity of the polypeptide remains unchanged. For example, an amino acid change may take place within a β -turn, away from the active site of the polypeptide. Also changes such as deletions (e.g. removal of a segment of the polypeptide, or in the corresponding nucleic acid sequence encoding such polypeptide, which does not affect the active site) and additions (e.g. addition of more peptides to the polypeptide sequence without affecting the function of the

active site, such as the formation of GST-fusion proteins, or additions in the corresponding nucleic acid sequence encoding such polypeptide without affecting the function of the active site) are also within the scope of the present invention. Such changes to the polypeptides can be performed by those with ordinary skill in the art using routine procedures and without undue experimentation. Thus, all possible nucleic and/or amino acid sequences that can readily be determined not to affect a significant activity of the peptide or protein of the invention are also fully described herein.

Other embodiments are within the following claims.

CLAIMS

What is claimed is:

1. An isolated, enriched, or purified nucleic acid molecule encoding an hWART polypeptide.
2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that
 - (a) encodes a polypeptide having the full length amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4;
 - (b) is the complement of the nucleotide sequence of (a);
 - (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring hWART polypeptide;
 - (d) encodes an hWART polypeptide having the full length amino acid sequence of the sequence set forth in SEQ ID NO:3 or SEQ ID NO:4, except that it lacks one or more of the following segments of amino acid residues:12-45, 55-151, 236-377, 404-520, 555-559, 601-702, 691-998, 1011-1086 of SEQ ID NO:3, or 1-33, 43-139, 342-466, 467-480, 514-518, 974-1048 of SEQ ID NO:4;
 - (e) is the complement of the nucleotide sequence of (d);
 - (f) encodes a polypeptide having the amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4 from amino acid residues 12-45, 55-151, 236-377, 404-520, 555-559, 601-702, 691-998, 1011-1086 of SEQ ID NO:3, or 1-33, 43-139, 342-466, 467-480, 514-518, 974-1048 of SEQ ID NO:4;

(g) is the complement of the nucleotide sequence of (f);

(h) encodes a polypeptide having the full length amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4, except that it lacks one or more of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, and a C-terminal domain; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

4. The nucleic acid molecule of claim 3, wherein said mammal is a human.

5. The nucleic acid molecule of claim 1, further comprising a vector or promoter effective to initiate transcription in a host cell.

6. A nucleic acid probe for the detection of nucleic acid encoding an hWART polypeptide in a sample.

7. The probe of claim 6 wherein said polypeptide comprises at least 46 contiguous amino acids of the amino acid sequence shown in SEQ ID NO:3 or SEQ ID NO:4.

8. A nucleic acid molecule comprising one or more regions that encode an hWART polypeptide or an hWART domain polypeptide, wherein said hWART polypeptide or said hWART domain polypeptide is fused to a non-WART polypeptide.

9. A recombinant cell comprising a nucleic acid molecule encoding either

- (a) an hWART polypeptide;
- (b) an hWART domain polypeptide; or
- (c) an hWART polypeptide or hWART domain polypeptide fused to a non-WART polypeptide.

10. An isolated, enriched or purified hWART polypeptide.

11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by the full length amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4.

12. The polypeptide of claim 10, wherein said polypeptide comprises an amino acid sequence having

- (a) the full length amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4;

- (b) the full length amino acid sequence of the sequence set forth in SEQ ID NO:3 or SEQ ID NO:4, except that it lacks one or more of the following segments of amino acid residues: 12-45, 55-151, 236-377, 404-520, 555-559, 601-702, 691-998, 1011-1086 of SEQ ID NO:3, or 1-33, 43-139, 342-466, 467-480, 514-518, 974-1048 of SEQ ID NO:4;

- (c) the amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4 from amino acid residues 12-45, 55-151, 236-377, 404-520, 555-559, 601-702, 691-998, 1011-1086 of SEQ ID NO:3, or 1-33, 43-139, 342-466, 467-480, 514-518, 974-1048 of SEQ ID NO:4; or

- (d) the full length amino acid sequence set forth in SEQ ID NO:3 or SEQ ID NO:4 except that it lacks one or more of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, and a C-terminal domain.

13. An antibody or antibody fragment having specific binding affinity to an hWART polypeptide or an hWART domain polypeptide.

14. A hybridoma which produces an antibody having specific binding affinity to an hWART polypeptide.

15. A method for identifying a substance capable of modulating hWART activity comprising the steps of:

- (a) contacting an hWART polypeptide with a test substance; and
- (b) determining whether said substance alters the activity of said polypeptide.

16. A method for identifying a substance capable of modulating hWART function in a cell comprising the steps of:

- (a) expressing an hWART polypeptide in a cell;
- (b) adding a test substance to said cell; and
- (c) monitoring a change in either cell phenotype, cell proliferation, cell differentiation, hWART catalytic activity, or the interaction between an hWART polypeptide and a natural binding partner.

17. A method of preventing or treating an abnormal condition by administering to a patient in need of such treatment a compound that modulates the function of an hWART polypeptide.

18. The method of claim 17, wherein said abnormal condition involves an abnormality in hWART signal transduction pathway.

19. The method of claim 18, wherein said abnormal condition is cancer.

20. The method of claim 17, wherein said compound modulates the function of an hWART polypeptide *in vitro*.

21. A kit, comprising the compound of claim 17 and a protocol for the use of said compound.

22. The kit of claim 21, wherein said protocol is approved by the Food and Drug Administration.

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Wart1_h	1		MRKSEKPEGYRQ	12
Wart2_h	1	MRPKTFPATYSGNSRQLQEIREGLKQPSKSSVQGLPAGPNSDTSLEDAKVLGSKDATRQ		60
Wart1_h	13	MRPKTFPASNYTVSSRQLQEIRESLRNLKSKPS-----DAAKAEHNM-----SKMSTED		61
Wart2_h	61	QQQMRATPKFGPYQKALREIRYSLLPFANESGTS-AAAENVNRQMLQELVNAGCDQEMAGR		119
Wart1_h	62	PRQVRNPPKFGTHHKALQEIRNSLLPFANETNSSRSTSEVNPQMLQDLQAAGFDEDMVIQ		121
Wart2_h	120	ALKQTGSRISIEAALEYISKMGYLDPRNEQIV---RVIKQT-SPGKGLMPTPVTRRPSFE		174
Wart1_h	122	ALQKTNNRSIEAAIEFISKMSYQDPRREQMAAAAARPINASMKGPN--VQQSVNRKQSWK		179
Wart2_h	175	GTGDSFASYHQLSGTPY-EGPSFGADGPTALEEMPRP-----YVDY-----LFP-		217
Wart1_h	180	GSKESLVP--QRHGPPLAESVAYHSESPNSQTDVGRPLSGSGISAFVQAHPSNGQRVNP		237
Wart2_h	218	-----GVGPHGPGHQHQHPPKG-----YGASVEAAGAHFPLQGAHYGR		255
Wart1_h	238	PPPQVRSVTPPPPPRGQTTPPRGTTPPPPSWEPNSTKRYSGNME-----YVI		285
Wart2_h	256	PHL--LVPGE-PLGYGVQRSPSFQS--KTTPETG--GYASLPTKGQ-----G		295
Wart1_h	286	SRISVPVPGAWQEGY---PPPLNTSMNPNPNQQRGISSVPVGRQPIIMQSSSKFNFP		342
Wart2_h	296	GPPG---AGLA-F-----PPPAAGLYVPHPHKQAGPAAHQHLVGLSRS		335
Wart1_h	343	GRPGMQNGTGQTDFMIHQNVVPAGTVNRQPPP-----PYPLTAANGQSPSALQTGGSAA		396
Wart2_h	336	QV-FASDSPQSLTTPSRNSLNVLDLYELGSTSVQ-QWPAATLARRDSLQKPGLEAPPRAH		393
Wart1_h	397	PSSYTNGSIPQSMVMVPNRNSHNMELYNTSVPLQTNWPOSSSAPAQSSPSSGHEIPTW--		454
Wart2_h	394	VAFRPDCVPVSRTNSFNSHQF---RPGPPGKAEPSPAPANTVTAVTAAHILHPVKSVRL		450
Wart1_h	455	---QPNIPV--RSNSFNN--PLGNRASHSANSQPS---ATTVTAITPAPIQQPVKSMRVL		504
Wart2_h	451	RPEPQTAVGSPHPAWVPAPAPAPAPAPAAEGLDAKEEHALALGGAGAFPLDVEYGGPD		510
Wart1_h	505	KPELQTLATAPHSWIPQPIQTVQPSPPF-----EGTASNVTVMPPVPEAP---NYQGP-		555
Wart2_h	511	RRCPPPPYPKHLRLSRKS-EWART1-HDLDSLCL-AGMEQ---SLRAGPNEPEGGDKSRKS-AKGDK		565
Wart1_h	556	---PPYPKHLHQNPVSPVPE--SISKPSKEDQPSL---PKE---DESEKSYENVDS		602
Wart2_h	566	GKDKKKQIQTSVPVVRKNRDEEKRESRIKSYSPYAFKFFMEQHVENVIKTYQQKVNRL		625
Wart1_h	603	GDKEKKQITTSPIVTRKNKKDEERRESRIQSYSPQAFKFFMEQHVENVLKSHQORLHRKK		662

FIG. 1A

		***** *****	
Wart2_h	626	QLEQEMAKAGLCAEQEQMRKILYQKESNYNRLKRAKMDKSMFVKIKITLGLIGAFGEVCLA	685
Wart1_h	663	QLENEMMRVGLSQDAQDQMRKMLCKQESNYIRLKRAKMDKSMFVKIKITLGLIGAFGEVCLA	722

Wart2_h	686	CKVDTHALYAMKTLRKKDVLNRNQVAHVKAERDILAEADNEWVVKLYYSFQDKDSLIFYVM	745
Wart1_h	723	RKVDTKALYATKTLRKKDVLNRNQVAHVKAERDILAEADNEWVRLYYSFQDKDNLIFYVM	782

Wart2_h	746	DYIPGGDMMSLLIRMEVFPEHLARFYIAELTLAIESVHKMGFIHRD IKPDN LILDRDGH I	805
Wart1_h	783	DYIPGGDMMSLLIRMGIFPESLARFYIAELTCAVESVHKMGFIHRD IKPDN LILDRDGH I	842

Wart2_h	806	KLTD FGLCTGFRWTHNSKYQKGSVHRQDSMEPSDLWDDVSNCRCGDRLKTLTEQRARKQH	865
Wart1_h	843	KLTD FGLCTGFRWTHDSKYQSGDHPRQDSMDFSNNEWGDPSSCRCGDRLKPLERRAARQH	902

Wart2_h	866	QRCLAHSLVGTPNYIAPEVLLRKGYTQLCDWWSVGVILFEMLVGQPPFLAPTPTETQLKV	925
Wart1_h	903	QRCLAHSLVGTPNYIAPEVLLRTGYTQLCDWWSVGVILFEMLVGQPPFLAQTPLETQMKV	962

Wart2_h	926	INWENTLHI PAQVKLSPEARDLITKLCCSADHRLGRNGADDLKAHPFFSAIDFSSDIRKQ	985
Wart1_h	963	INWQTSLHI PPQAKLSPEASDLIIKLCRGPEDRLGKNGADEIKAHPPFKTIDFSSDLRQQ	1022

Wart2_h	986	PAPYVPTISHPMDTSNFPDVPDEESPWNDASEGSTKAWDTLTS--PNNKHPEHAFYEFTFR	1043
Wart1_h	1023	SASYIPKITHPTDTSNFPDVPDPKLWSDDNEEENVN-DTLNGWYKNGKHPEHAFYEFTFR	1081

Wart2_h	1044	RFFDDNGYPFRCPKPSGAEASQAESSDLESSDLVDQTEGCQ----PVYY	1088
Wart1_h	1082	RFFDDNGYPYNPKPIEYEYINSQGEQOSDE-DDONTGSEIKNRDLVYY	1130

FIG. 1B

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Wartl_h	1		MKRSEKFE	8
Wart_dm	1		MHPAGEKRGGRPNPKYTAEALES	23
Wartl_h	9	GYRQMRPKTFPASNYTVSSRQMLQEIRESLRNLSKPSDAAKAEHNMSKMSTEDPRQVRNP		68
Wart_dm	24	IKQDLTRFEVQNNHRNNQNYTPLYTATNGRNDALTPDYHHAKQFMEPPPSASPAPDVVI		83
Wartl_h	69	PKFGTHHKALQEIIRNSLLPFANETNSSRSTSEVNPQMLQDLQAAGFDEDMVIQALQKTNN		128
Wart_dm	84	PPPPAIVGQPGAGSISVSGVGVGVGVANGRVPKMMTALMPNKLIRKPSIERDTASSHYL		143
Wartl_h	129	RSIEAAIEFISKMSYQDPRREQMAAAAARPINASMKPGNVQQSVNRKQSWKGSKESLVPQ		188
Wart_dm	144	RCSPALDSGAGSSRSDSPHSHHTHQPSRT-VGNPGGNGGFS-----PSP		187
Wartl_h	189	RHGPPLAESV-----AYHSESPNSQTDVGRPLSGSGISAFVQAHPSNGQRVNPPPP		239
Wart_dm	188	SGFSEVAPPAPPPRNPTASS-AATPPPPV-PPTSQA-----YVKRR-----		226
Wartl_h	240	PQVRSVTPP-PPPRGQTPPPRGTTPPPPSWEPNSQTKRYSGNMEYVISRISPVPPGAWQE		298
Wart_dm	227	---SPALNNRPPAIAPPTQ--RGNS-----PVITQN-----GLKNPQQQ---		260
Wartl_h	299	GYPPLNTSP--MNPPNQGQRGISSVPVGRQPIIMQSSSKFNFPSGRPGMQNGTGQTDf		356
Wart_dm	261	LTQQLKSLNLYPGGGSGAVV-EPppPYLIQGGAGGAAPP-----PPPSYTA-----S		307
Wartl_h	357	MIHQ----NVVP---AGTVNRQPPPPYPLTA-ANGQSPSALQTGGSAAPSSYTNGSIPQS		408
Wart_dm	308	M-----QSRQSPQSQSDYRKSPSSG-----		329
Wartl_h	409	MMVPNRNShNMELYNISVPLQTNWPQSSSAPAQS-----SPSSGHEIPTWQPNIFVR		461
Wart_dm	330	-----IYSATSAGSPSPITVSLPPAPLAKPQPRVYQARSQQPIIMQSVKSTQV		377
Wartl_h	462	SNSFNNPLGNRASHSANSQPSATTVT-AITPAI-----QQP-----VKSMRV		503
Wart_dm	378	QKPVLTAVAPQSPSSASNSPVHVLAAPPSYPKSAAVVQQQQQAAAAAHQQHQHQ		437
Wartl_h	504	LKPELTALAPTHPSWIPQPIQTVQ----PSPFEGTASNVTVMPPVAEAPNYQ-----		553
Wart_dm	438	SKPATPTTPPLVGLNSKPNCLEPPSYAKSMQAKAATVVQQQQQQQQQQVQQQQVQQQQQ		497
Wartl_h	554	-----GP-----PPPYPK-----HLLHQ--		556
Wart_dm	498	QQQQQLQALRVLQAQAQRERDQERERDQKLANGNPGRQMLPPPPYQSNNNNNSEIKPP		557
Wartl_h	567	-----NPS-----VPPYES-----		575

FIG. 2A

FIG. 2B

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Plowman, Gregory
Flanagan, Peter
- (ii) TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSEQ for Windows 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Warburg, Richard J.
(B) REGISTRATION NUMBER: 32,327
(C) REFERENCE/DOCKET NUMBER: 224/006
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (213) 489-1600
(B) TELEFAX: (213) 955-0440
(C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CAGCGGAGTG	CGGCGGCGGC	GACACTGAGT	GGAAAGGCAAA	ATGGCGGCGG	CGGCGGCGGT	60
GGCCTGGTGT	TAAGGGGAGA	GCCAGGTCCCT	CACGACCCCT	GGGACGGGCC	GCGCTGGCCC	120
GCGGCAGCCC	CCCCGTTCGT	CTCCCCGCTC	TGCCCCACCA	GGGATACTTG	GGGTTGCTGG	180
GACGGACTCT	GGCCGCCTCA	GCGTCCGCCC	TCAGGCCCGT	GGCCGCTGTC	CAGGAGCTCT	240
GCTCTCCCTT	CCAGAGTTAA	TTATTTATAT	TGTAAGAAT	TTTAACAGTC	CTGGGGACTT	300
CCTTGAAGGA	TCATTTTCAC	TTTGTCTCAG	AAGAAAGCTC	TGGATCTATC	AAATAAAGAA	360
GTCCTTCGTG	TGGGCTACAT	ATATAGATGT	TTTCATGAAG	AGGAGTGAAA	AGCCAGAAGG	420
ATATAGACAA	ATGAGGCCTA	AGACCTTTCC	TGCCAGTAAC	TATACTGTCA	GTAGCCGGCA	480
AATGTTACAA	GAAATTCGGG	AATCCCTTAG	GAATTTATCT	AAACCATCTG	ATGCTGCTAA	540
GGCTGAGCAT	AACATGAGTA	AAATGTCAAC	CGAAGATCCT	CGACAAGTCA	GAAATCCACC	600
CAAATTTGGG	ACGCATCATA	AAGCCTTGCA	GGAAATTCGA	AACCTCTCTG	TTCCATTGTC	660
AAATGAAACA	AATTCCTCTC	GGAGTACTTC	AGAAGTTAAT	CCACAAATGC	TTCAAGACTT	720
GCAAGCTGCT	GGATTTGATG	AGGATATGGT	TATACAAGCT	CTTCAGAAAA	CTAACAACAG	780
AAGTATAGAA	GCAGCAATTG	AATTCATTAG	TAAAATGAGT	TACCAAGATC	CTCGACGAGA	840
GCAGATGGCT	GCAGCAGCTG	CCAGACCTAT	TAATGCCAGC	ATGAAACCAG	GGAATGTGCA	900
GCAATCAGTT	AACCGCAAAC	AGAGCTGGAA	AGGTTCTAAA	GAATCCTTAG	TTCTCTAGAG	960
GCATGGCCCG	CCACTAGCAG	AAAGTGTGGC	CTATCATTCT	GAGAGTCCCA	ACTCACAGAC	1020
AGATGTAGGA	AGACCTTTGT	CTGGATCTGG	TATATCAGCA	TTTGTTCAG	CTCACCCTAG	1080
CAACGGACAG	AGAGTGAACC	CCCCACCACC	ACCTCAAGTA	AGGAGTGTTA	CTCCTCCACC	1140
ACCTCCAAGA	GGCCAGACTC	CCCTCCCAAG	AGGTACAAC	CCACCTCCCC	CTTCATTGGA	1200
ACCAAACCTCT	CAAAACAAGC	GCTATTCTGG	AAACATGGAA	TACGTAATCT	CCCGAATCTC	1260
TCTGTCCCCA	CCTGGGGCAT	GGCAAGAGGG	CTATCTCTCA	CCACCTCTCA	ACACTTCCCC	1320
CATGAATCCT	CCTAATCAAG	GACAGAGAGG	CATTAGTTCT	GTTCCTGTTG	GCAGACAACC	1380
AATCATCATG	CAGAGTTCTA	GCAAATTTAA	CTTTCCATCA	GGGAGACCTG	GAATGCAGAA	1440
TGGTACTGGA	CAAACTGATT	TCATGATACA	CCAAAATGTT	GTCCCTGCTG	GCATCTGTAA	1500
TCGGCAGCCA	CCACCTCCAT	ATCCTCTGAC	AGCAGCTAAT	GGACAAAGCC	CTTCTGCTTT	1560
ACAAACAGGG	GGATCTGCTG	CTCCTTCGTC	ATATACAAAT	GGAAAGTATTC	CTCAGTCTAT	1620
GATGGTGCCA	AACAGAAATA	GTCATAACAT	GGAACTATAT	AACATTAGTG	TACCTGGACT	1680
GCAAACAAAT	TGGCCTCAGT	CATCTTCTGC	TCCAGCCGAG	TCATCCCCGA	GCAGTGGGCA	1740
TGAAATCCCT	ACATGGCAAC	CTAACATACC	AGTGAGGTCA	AATCTTTTTA	ATAACCCATT	1800
AGGAAATAGA	GCAAGTCACT	CTGCTAATTC	TCAGCCTTCT	GCTACAACAG	TCAGTGCAT	1860
TACACCAGCT	CCTATTCAAC	AGCCTGTGAA	AAGTATGCGT	GTATTAATAA	CAGAGTACAA	1920
GACTGCTTTA	GCACCTACAC	ACCCTTCTTG	GATACCACAG	CCAATTCAAA	CTGTTCAACC	1980
CAGTCTTTTT	CCTGAGGGAA	CCGCTTCAAA	TGTGACTGTG	ATGCCACCTG	TTGCTGAAGC	2040
TCCAAACTAT	CAAGGACCAC	CACCACCCTA	CCCAAAACAT	CTGCTGCACC	AAAACCCATC	2100
TGTTCTCCA	TACGAGTCAA	TCAGTAAGCC	TAGCAAAGAG	GATCAGCCAA	GCTTGCCCAA	2160
GGAAGATGAG	AGTGAAAAGA	GTTATGAAAA	TGTTGATAGT	GGGGATAAAG	AAAAGAAACA	2220
GATTACAAC	TCACCTATTA	CTGTTAGGAA	AAACAAGAAA	GATGAAGAGC	GAAGGGAATC	2280
TCGTATTCAA	AGTTATTCTC	CTCAAGCATT	TAAATCTTTT	ATGGAGCAAC	ATGTAGAAAA	2340
TGTACTCAA	TCTCATCAGC	AGCGTCTACA	TGTAAAAAAA	CAATTAGAGA	ATGAAATGAT	2400
GCGGTTGGA	TTATCTCAAG	ATGCCAGGGA	TCAAATGAGA	AAGATGCTTT	GCCAAAAAGA	2460
ATCTAATTAC	ATCCGTCTTA	AAAGGGCTAA	AATGGACAAG	TCTATGTTTG	TGAAGATAAA	2520
GACACTAGGA	ATAGGAGCAT	TTGGTGAAGT	CTGTCTAGCA	AGAAAAAGTAG	ATACTAAGGC	2580
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TGTTAAGGCT	GAGAGAGATA	TCCTGGCTGA	AGCTGACAAT	GAATGGGTAG	TTCTGCTATA	2700
TTATTCAATC	CAAGATAAGG	ACAATTTATA	CTTTGTAATG	GACTACATTC	CTGGGGGTGA	2760
TATGATGAGC	CTATTAATTA	GAATGGGCAT	CTTTCCAGAA	AGTCTGGCAC	GATTCTACAT	2820
AGCAGAAGTT	ACCTGTGCAG	TTGAAAGTCT	TCATAAAATG	GGTTTTATTG	ATAGAGATAT	2880
TAAACCTGAT	AATATTTTGA	TTGATCGTGA	TGGTCATATT	AAATTGACTG	ACTTTGGCCT	2940
CTGCACTGGC	TTCAGATGGA	CACACGATTC	TAACTACTAT	CAGAGTGGTG	ACCATCCACG	3000
GCAAGATAGC	ATGGATTTCA	GTAATGAATG	GGGGGATCCC	TCAAGCTGTC	GATGTGGAGA	3060
CAGACTGAAG	CCATTAGAGC	GGAGAGCTGC	ACGCCAGCAC	CAGCGATGTC	TAGCACATTC	3120
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TTTCTTGGCA	CAAAACCAT	TAGAAACACA	AATGAAGGTT	ATCAACTGGC	AAACATCTCT	3300
TCACATTCCA	CCACAAGCTA	AATCAGTCC	TGAAGCTTCT	GATCTTATTA	TTAACTTTG	3360

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TGATGATAAC	GAGGAAGAAA	ATGTAAATGA	CACCTCTCAAT	GGATGGTATA	AAAAATGGAAA	3600
GCATCCTGAA	CATGCATTCT	ATGAATTTAC	CTTCCGAAGG	TTTTTTGATG	ACAATGGCTA	3660
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TATTATAGTC	AGTTCTTGGT	ACTTAAAGTA	CTTAAATAAA	GTAGTGCTTT	GTTTAAAAGG	4080
AGAAACCTGG	TATCTATTTG	TATATATGCT	AAATAAATTT	AAAATACAAG	AGTTTATTGA	4140
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CCTGAAACTA	AGGAATACAG	GGTTGAAAAA	ATATTAATAT	GTTTGTGAGA	AGGAAAAATA	4380
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TCTGGCAATA	TTTTACCTAA	GCGCAGATTA	ATTGGTGAAA	AAATTAACCT	TTAAGATGGC	4800
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AAGGCAGAGT	TGTTGCAGTT	GAATTGGAGA	TTAGGGCAA	AGAACACTTA	TTAGCCACAA	5220
CTTCCACCTT	TTCTACAGGT	GGTCCCTTCA	GAGCTCAGCC	TGAAAACCCA	CTACTGTGTT	5280
ATCGTGCCTG	TTTTGGGGTT	AGTGGTCTCT	TTGAGAACTT	GAAGGAAGCT	TGGGACTCTT	5340
CCTAGAAAAA	AAAACACAC	ATACACATAC	AATGTTGCAT	GCAGTTTCAA	GGGATTTTGG	5400
ACATATTGAA	ACCTATCACA	GGCTGTAGGT	TATGGACCTC	TGTGCCATGA	GAAAATTGAT	5460
ACATTTAACT	AAGAACTTTG	TTTTTAACTT	ACCAATCACT	ACTCAGCACA	TCTTATATAA	5520
CGTGATAAAT	TGTGATGGAA	AAGGTCTGTA	GCATGTGATA	TAAGGTGACC	TTATGAATGC	5580
CTCTCTTGCT	GGTACATTAA	GTTGTTTTAA	TATATCATTT	GGAGGGGACT	GAAATGTTAG	5640
GCTCATTACA	AGCTTGATAC	AGAAATATTT	CTGAAGGATT	TCTAATCAGA	ATTGTAAGAC	5700
AATGTGCTAT	CATGAAATCG	CAGTCTTCAC	CTCATGGTTC	ATGGAACATT	TGGTTAGTCC	5760
CATAAAATCC	TATGCAAAAC	AAAGTAGTTC	AAGAAATTTT	AGGTGGGTAG	TCACATTTAT	5820
AAGGTATTCT	TCTTACTCTT	TGGGCTTTTT	CAGTCTGATT	TATTTAAATT	TTCAATTTAGT	5880
TGTTTTACTT	TTGGACTAAG	GTGCAATACA	ACTTTGTTAC	ACTTTGTTAC	ATTTATGTTG	5940
TAGGAAAACT	AAGGTGCTGT	CTCCTCCCCC	TTCCCTTCCC	ACAAAATCTG	TATTTCCCTT	6000
ATTGCTGAAA	TGTAACAGAC	ACTACAAATT	TTGTATTCTT	TTTTTGTTTT	TTGTTTTGAG	6060
ACAGGGTCTC	ACTCTGTCAC	CCAGGCTGGA	GGGCAGTGGC	GCTTCACAGC	TCACATGCATC	6120
CTCAACCTTG	GGGCTCAGC	CAGTCCCTCC	GCCTCAGCCT	CCCAAGTAGC	TGGGCATGCG	6180
CCACCAAGCC	CAGCTAATTT	TTGTATCTTT	AGTAGAGATG	GGGTTTCGCC	ATGTTGCCCA	6240
GGTTGGTGTG	GAATTCCTGG	GCTCCAGTTA	TATGCCACCC	TCAGCCTCCC	AAAGTGCTGG	6300
GATTACAGAC	GTGACCCACC	GCGCCTGGCG	CAAAATATGTA	TTCTTTTAAA	ATTTCTCTCTG	6360
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TAACAGTTTG	GATATACTTA	TCAGCTATCT	TATTTCCAAA	CTACATCTAC	TTCTTCCAGT	6480
ATAGAATCTG	GTGCTTCCCTG	ACCAAAAAGA	TGAGAAAAAC	AATGTTAAAA	ATATAGATGC	6540
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AAGATGTGTT	CTATAATTAT	GTAATTGTAG	ATACTGTTAT	GCATTGTCCA	GTGACATCAT	6720
AAGGCAGGCC	CTACTGCTGT	ATCTTTTCTA	CCTTCTTATT	TGTAATAGAA	ACTATAGAA	6780
GTATGACTAA	AAAGTCACTT	TGAGATTGAC	TTTTTTAAAA	AGTTATTACC	TTCTGCTGTT	6840
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GAATACAGTG	GGAGGATTTT	TAGACATTGC	TGCTGCTGTT	ACCCAAGGTA	TTTTAGATAA	6960
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ATCTAAAGCA	AAAAGTAATT	TGGGTCAAAA	TATTGSTATA	TTTGTAAGGC	GCCTTAATAT	7080
ATCCCTTTGT	GGAAGGCAT	ACACAGTTTA	CTTTTATATT	GTATTGTGTA	TATAAGTATT	7140
TTGTATTAAA	ATTGAATCAG	TGGCAACATT	AAAGTTTTAT	AAAATCATGC	TTTGTAGAA	7200
AAAGAATTAC	AGCTTTGCAA	TATAACTAAT	TGTTTCGCAT	AATTTCTGAAT	GTAATAGATA	7260
TGAATAATCA	GCCTGTGTTT	TTAATGAACT	TATTTGTATT	TTCCCAATCA	TTTTCTCTAG	7320
TGTAATGTTT	GCTGGGATAA	TAAAAAAAAT	TCAATCTTTT	CGAAAAAAA	AAAAAAA	7380
AA						7382

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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GGGAGCGGCC GGCCAGGACG CCCCAGGGG TGTAGACCGC GCCCCCTGGA GAGAGTGATA 180
ATCTTCAAAA TGAAGACTTT GGAAATTTT AGGTTCTCTA TAGGAAC TAC AAAAAATGGA 240
GGAAAGAAAC TTTTCAAAAG GAAATTATTT TGAAAGTATG TTTACAACAA ACTGATACTA 300
TTGACAGTTT TTTTTTTAAA TAATAAAACA CTTTAAGAAG ATTGTATTTA TGGTAAAAGG 360
AAACTGGACT AACAAATGAG CCAAAGACTT TTCCTGCCAC GACTTATTCT GGAAATAGCC 420
GGCAGCGACT GCAAGAGATT CGTGAGGGGT TAAAGCAGCC ATCCAAGTCT TCGGTTTCAGG 480
GGCTACCCGC AGGACCAAAC AGTGACACTT CCCTGGATGC CAAAGTCCTG GGGAGCAAAG 540
ATGCCACCAG GCAGCAGCAG CAGATGAGAG CCACCCCAAA GTTCGGACCT TATCAGAAAG 600
CCTTGAGGGA AATCAGATAT TCCTTGTTGC CTTTGTCTAA TGAATCGGGC ACCTCTGCAG 660
CTGCAGAGT GAACCGGCAA ATGCTGCAGG AACTGGTGAA CGCAGGATGC GACCAGGAGA 720
TGGCTGGCCG AGCTCTCAAG CAGACTGGCA GCAGGAGCAT CGAGGCCGCC CTGGAGTACA 780
TCAGCAAGAT GGGCTACCTG GACCCGAGGA ATGAGCAGAT TGTGCGGGTC ATTAAGCAGA 840
CCTCCCCAGG AAAGGGGCTC ATGCCAACCC CAGTGACCGG GAGGCCCAGC TTCGAAGGAA 900
CCGGCGATTG GTTTGCGTCC TACCACCAGC TGAGCGGTAC CCCCTACGAG GGCCCAAGCT 960
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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1130 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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Met Lys Arg Ser Glu Lys Pro Glu Gly Tyr Arg Gln Met Arg Pro Lys
 1          5          10          15
Thr Phe Pro Ala Ser Asn Tyr Thr Val Ser Ser Arg Gln Met Leu Gln
 20          25          30
Glu Ile Arg Glu Ser Leu Arg Asn Leu Ser Lys Pro Ser Asp Ala Ala
 35          40          45
Lys Ala Glu His Asn Met Ser Lys Met Ser Thr Glu Asp Pro Arg Gln
 50          55          60
Val Arg Asn Pro Pro Lys Phe Gly Thr His His Lys Ala Leu Gln Glu
 65          70          75          80
Ile Arg Asn Ser Leu Leu Pro Phe Ala Asn Glu Thr Asn Ser Ser Arg
 85          90          95

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Ser Thr Ser Glu Val Asn Pro Gln Met Leu Gln Asp Leu Gln Ala Ala
 100 105 110
 Gly Phe Asp Glu Asp Met Val Ile Gln Ala Leu Gln Lys Thr Asn Asn
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 Arg Ser Ile Glu Ala Ala Ile Glu Phe Ile Ser Lys Met Ser Tyr Gln
 130 135 140
 Asp Pro Arg Arg Glu Gln Met Ala Ala Ala Ala Arg Pro Ile Asn
 145 150 155 160
 Ala Ser Met Lys Pro Gly Asn Val Gln Gln Ser Val Asn Arg Lys Gln
 165 170 175
 Ser Trp Lys Gly Ser Lys Glu Ser Leu Val Pro Gln Arg His Gly Pro
 180 185 190
 Pro Leu Ala Glu Ser Val Ala Tyr His Ser Glu Ser Pro Asn Ser Gln
 195 200 205
 Thr Asp Val Gly Arg Pro Leu Ser Gly Ser Gly Ile Ser Ala Phe Val
 210 215 220
 Gln Ala His Pro Ser Asn Gly Gln Arg Val Asn Pro Pro Pro Pro Pro
 225 230 235 240
 Gln Val Arg Ser Val Thr Pro Pro Pro Pro Pro Arg Gly Gln Thr Pro
 245 250 255
 Pro Pro Arg Gly Thr Thr Pro Pro Pro Pro Ser Trp Glu Pro Asn Ser
 260 265 270
 Gln Thr Lys Arg Tyr Ser Gly Asn Met Glu Tyr Val Ile Ser Arg Ile
 275 280 285
 Ser Pro Val Pro Pro Gly Ala Trp Gln Glu Gly Tyr Pro Pro Pro Pro
 290 295 300
 Leu Asn Thr Ser Pro Met Asn Pro Pro Asn Gln Gly Gln Arg Gly Ile
 305 310 315 320
 Ser Ser Val Pro Val Gly Arg Gln Pro Ile Ile Met Gln Ser Ser Ser
 325 330 335
 Lys Phe Asn Phe Pro Ser Gly Arg Pro Gly Met Gln Asn Gly Thr Gly
 340 345 350
 Gln Thr Asp Phe Met Ile His Gln Asn Val Val Pro Ala Gly Thr Val
 355 360 365
 Asn Arg Gln Pro Pro Pro Pro Tyr Pro Leu Thr Ala Ala Asn Gly Gln
 370 375 380
 Ser Pro Ser Ala Leu Gln Thr Gly Gly Ser Ala Ala Pro Ser Ser Tyr
 385 390 395 400
 Thr Asn Gly Ser Ile Pro Gln Ser Met Met Val Pro Asn Arg Asn Ser
 405 410 415
 His Asn Met Glu Leu Tyr Asn Ile Ser Val Pro Gly Leu Gln Thr Asn
 420 425 430
 Trp Pro Gln Ser Ser Ser Ala Pro Ala Gln Ser Ser Pro Ser Ser Gly
 435 440 445
 His Glu Ile Pro Thr Trp Gln Pro Asn Ile Pro Val Arg Ser Asn Ser

450	455	460
Phe 465	Asn 470	Asn 475
Pro 485	Ser 490	His 495
Pro 500	Val 505	Leu 510
Ala 515	Pro 520	Gln 525
Pro 530	Thr 535	Val 540
Pro 545	Val 550	Pro 555
Lys 565	His 570	Pro 575
Ser 580	Lys 585	Pro 590
Ser 595	Glu 600	Lys 605
Gln 610	Ile 615	Thr 620
Glu 625	Arg 630	Ser 635
Phe 645	His 650	Val 655
Arg 660	Lys 665	Met 670
Leu 675	Asp 680	Met 685
Glu 690	Asn 695	Met 700
Phe 705	Lys 710	Ala 715
Leu 725	Thr 730	Thr 735
Arg 740	Val 745	His 750
Glu 755	Ile 760	Val 765
Tyr 770	Lys 775	Phe 780
Ile 785	Met 790	Arg 795
Pro 805	Arg 810	Val 815

Glu Ser Val His Lys Met Gly Phe Ile His Arg Asp Ile Lys Pro Asp
 820 825 830
 Asn Ile Leu Ile Asp Arg Asp Gly His Ile Lys Leu Thr Asp Phe Gly
 835 840 845
 Leu Cys Thr Gly Phe Arg Trp Thr His Asp Ser Lys Tyr Tyr Gln Ser
 850 855 860
 Gly Asp His Pro Arg Gln Asp Ser Met Asp Phe Ser Asn Glu Trp Gly
 865 870 875 880
 Asp Pro Ser Ser Cys Arg Cys Gly Asp Arg Leu Lys Pro Leu Glu Arg
 885 890 895
 Arg Ala Ala Arg Gln His Gln Arg Cys Leu Ala His Ser Leu Val Gly
 900 905 910
 Thr Pro Asn Tyr Ile Ala Pro Glu Val Leu Leu Arg Thr Gly Tyr Thr
 915 920 925
 Gln Leu Cys Asp Trp Trp Ser Val Gly Val Ile Leu Phe Glu Met Leu
 930 935 940
 Val Gly Gln Pro Pro Phe Leu Ala Gln Thr Pro Leu Glu Thr Gln Met
 945 950 955 960
 Lys Val Ile Asn Trp Gln Thr Ser Leu His Ile Pro Pro Gln Ala Lys
 965 970 975
 Leu Ser Pro Glu Ala Ser Asp Leu Ile Ile Lys Leu Cys Arg Gly Pro
 980 985 990
 Glu Asp Arg Leu Gly Lys Asn Gly Ala Asp Glu Ile Lys Ala His Pro
 995 1000 1005
 Phe Phe Lys Thr Ile Asp Phe Ser Ser Asp Leu Arg Gln Gln Ser Ala
 1010 1015 1020
 Ser Tyr Ile Pro Lys Ile Thr His Pro Thr Asp Thr Ser Asn Phe Asp
 1025 1030 1035 1040
 Pro Val Asp Pro Asp Lys Leu Trp Ser Asp Asp Asn Glu Glu Glu Asn
 1045 1050 1055
 Val Asn Asp Thr Leu Asn Gly Trp Tyr Lys Asn Gly Lys His Pro Glu
 1060 1065 1070
 His Ala Phe Tyr Glu Phe Thr Phe Arg Arg Phe Phe Asp Asp Asn Gly
 1075 1080 1085
 Tyr Pro Tyr Asn Tyr Pro Lys Pro Ile Glu Tyr Glu Tyr Ile Asn Ser
 1090 1095 1100
 Gln Gly Ser Glu Gln Gln Ser Asp Glu Asp Asp Gln Asn Thr Gly Ser
 1105 1110 1115 1120
 Glu Ile Lys Asn Arg Asp Leu Val Tyr Val
 1125 1130

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

9

(A) LENGTH: 1088 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

Met Arg Pro Lys Thr Phe Pro Ala Thr Thr Tyr Ser Gly Asn Ser Arg
 1      5      10      15
Gln Arg Leu Gln Glu Ile Arg Glu Gly Leu Lys Gln Pro Ser Lys Ser
 20      25      30
Ser Val Gln Gly Leu Pro Ala Gly Pro Asn Ser Asp Thr Ser Leu Asp
 35      40      45
Ala Lys Val Leu Gly Ser Lys Asp Ala Thr Arg Gln Gln Gln Gln Met
 50      55      60
Arg Ala Thr Pro Lys Phe Gly Pro Tyr Gln Lys Ala Leu Arg Glu Ile
 65      70      75      80
Arg Tyr Ser Leu Leu Pro Phe Ala Asn Glu Ser Gly Thr Ser Ala Ala
 85      90      95
Ala Glu Val Asn Arg Gln Met Leu Gln Glu Leu Val Asn Ala Gly Cys
100      105      110
Asp Gln Glu Met Ala Gly Arg Ala Leu Lys Gln Thr Gly Ser Arg Ser
115      120      125
Ile Glu Ala Ala Leu Glu Tyr Ile Ser Lys Met Gly Tyr Leu Asp Pro
130      135      140
Arg Asn Glu Gln Ile Val Arg Val Ile Lys Gln Thr Ser Pro Gly Lys
145      150      155      160
Gly Leu Met Pro Thr Pro Val Thr Arg Arg Pro Ser Phe Glu Gly Thr
165      170      175
Gly Asp Ser Phe Ala Ser Tyr His Gln Leu Ser Gly Thr Pro Tyr Glu
180      185      190
Gly Pro Ser Phe Gly Ala Asp Gly Pro Thr Ala Leu Glu Glu Met Pro
195      200      205
Arg Pro Tyr Val Asp Tyr Leu Phe Pro Gly Val Gly Pro His Gly Pro
210      215      220
Gly His Gln His Gln His Pro Pro Lys Gly Tyr Gly Ala Ser Val Glu
225      230      235      240
Ala Ala Gly Ala His Phe Pro Leu Gln Gly Ala His Tyr Gly Arg Pro
245      250      255
His Leu Leu Val Pro Gly Glu Pro Leu Gly Tyr Gly Val Gln Arg Ser
260      265      270
Pro Ser Phe Gln Ser Lys Thr Pro Pro Glu Thr Gly Gly Tyr Ala Ser
275      280      285
Leu Pro Thr Lys Gly Gln Gly Gly Pro Pro Gly Ala Gly Leu Ala Phe
290      295      300
Pro Pro Pro Ala Ala Gly Leu Tyr Val Pro His Pro His His Lys Gln
305      310      315      320

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Ala	Gly	Pro	Ala	Ala	His	Gln	Leu	His	Val	Leu	Gly	Ser	Arg	Ser	Gln
			325						330					335	
Val	Phe	Ala	Ser	Asp	Ser	Pro	Pro	Gln	Ser	Leu	Leu	Thr	Pro	Ser	Arg
			340					345					350		
Asn	Ser	Leu	Asn	Val	Asp	Leu	Tyr	Glu	Leu	Gly	Ser	Thr	Ser	Val	Gln
		355					360					365			
Gln	Trp	Pro	Ala	Ala	Thr	Leu	Ala	Arg	Arg	Asp	Ser	Leu	Gln	Lys	Pro
	370					375					380				
Gly	Leu	Glu	Ala	Pro	Pro	Arg	Ala	His	Val	Ala	Phe	Arg	Pro	Asp	Cys
385					390					395				400	
Pro	Val	Pro	Ser	Arg	Thr	Asn	Ser	Phe	Asn	Ser	His	Gln	Pro	Arg	Pro
				405					410					415	
Gly	Pro	Pro	Gly	Lys	Ala	Glu	Pro	Ser	Leu	Pro	Ala	Pro	Asn	Thr	Val
			420					425					430		
Thr	Ala	Val	Thr	Ala	Ala	His	Ile	Leu	His	Pro	Val	Lys	Ser	Val	Arg
		435					440					445			
Val	Leu	Arg	Pro	Glu	Pro	Gln	Thr	Ala	Val	Gly	Pro	Ser	His	Pro	Ala
	450					455					460				
Trp	Val	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala
465					470					475					480
Ala	Glu	Gly	Leu	Asp	Ala	Lys	Glu	Glu	His	Ala	Leu	Ala	Leu	Gly	Gly
				485					490					495	
Ala	Gly	Ala	Phe	Pro	Leu	Asp	Val	Glu	Tyr	Gly	Gly	Pro	Asp	Arg	Arg
			500					505					510		
Cys	Pro	Pro	Pro	Pro	Tyr	Pro	Lys	His	Leu	Leu	Leu	Arg	Ser	Lys	Ser
		515					520					525			
Glu	Gln	Tyr	Asp	Leu	Asp	Ser	Leu	Cys	Ala	Gly	Met	Glu	Gln	Ser	Leu
	530					535					540				
Arg	Ala	Gly	Pro	Asn	Glu	Pro	Glu	Gly	Gly	Asp	Lys	Ser	Arg	Lys	Ser
545					550					555					560
Ala	Lys	Gly	Asp	Lys	Gly	Gly	Lys	Asp	Lys	Lys	Gln	Ile	Gln	Thr	Ser
				565					570					575	
Pro	Val	Pro	Val	Arg	Lys	Asn	Ser	Arg	Asp	Glu	Glu	Lys	Arg	Glu	Ser
			580					585					590		
Arg	Ile	Lys	Ser	Tyr	Ser	Pro	Tyr	Ala	Phe	Lys	Phe	Phe	Met	Glu	Gln
		595					600					605			
His	Val	Glu	Asn	Val	Ile	Lys	Thr	Tyr	Gln	Gln	Lys	Val	Asn	Arg	Arg
	610					615					620				
Leu	Gln	Leu	Glu	Gln	Glu	Met	Ala	Lys	Ala	Gly	Leu	Cys	Glu	Ala	Glu
625					630					635					640
Gln	Glu	Gln	Met	Arg	Lys	Ile	Leu	Tyr	Gln	Lys	Glu	Ser	Asn	Tyr	Asn
				645					650					655	
Arg	Leu	Lys	Arg	Ala	Lys	Met	Asp	Lys	Ser	Met	Phe	Val	Lys	Ile	Lys
			660					665					670		
Thr	Leu	Gly	Ile</												

Asp Thr His Ala Leu Tyr Ala Met Lys Thr Leu Arg Lys Lys Asp Val
 690 695 700
 Leu Asn Arg Asn Gln Val Ala His Val Lys Ala Glu Arg Asp Ile Leu
 705 710 715 720
 Ala Glu Ala Asp Asn Glu Trp Val Val Lys Leu Tyr Tyr Ser Phe Gln
 725 730 735
 Asp Lys Asp Ser Leu Tyr Phe Val Met Asp Tyr Ile Pro Gly Gly Asp
 740 745 750
 Met Met Ser Leu Leu Ile Arg Met Glu Val Phe Pro Glu His Leu Ala
 755 760 765
 Arg Phe Tyr Ile Ala Glu Leu Thr Leu Ala Ile Glu Ser Val His Lys
 770 775 780
 Met Gly Phe Ile His Arg Asp Ile Lys Pro Asp Asn Ile Leu Ile Asp
 785 790 795 800
 Leu Asp Gly His Ile Lys Leu Thr Asp Phe Gly Leu Cys Thr Gly Phe
 805 810 815
 Arg Trp Thr His Asn Ser Lys Tyr Tyr Gln Lys Gly Ser His Val Arg
 820 825 830
 Gln Asp Ser Met Glu Pro Ser Asp Leu Trp Asp Asp Val Ser Asn Cys
 835 840 845
 Arg Cys Gly Asp Arg Leu Lys Thr Leu Glu Gln Arg Ala Arg Lys Gln
 850 855 860
 His Gln Arg Cys Leu Ala His Ser Leu Val Gly Thr Pro Asn Tyr Ile
 865 870 875 880
 Ala Pro Glu Val Leu Leu Arg Lys Gly Tyr Thr Gln Leu Cys Asp Trp
 885 890 895
 Trp Ser Val Gly Val Ile Leu Phe Glu Met Leu Val Gly Gln Pro Pro
 900 905 910
 Phe Leu Ala Pro Thr Pro Thr Glu Thr Gln Leu Lys Val Ile Asn Trp
 915 920 925
 Glu Asn Thr Leu His Ile Pro Ala Gln Val Lys Leu Ser Pro Glu Ala
 930 935 940
 Arg Asp Leu Ile Thr Lys Leu Cys Cys Ser Ala Asp His Arg Leu Gly
 945 950 955 960
 Arg Asn Gly Ala Asp Leu Lys Ala His Pro Phe Phe Ser Ala Ile
 965 970 975
 Asp Phe Ser Ser Asp Ile Arg Lys Gln Pro Ala Pro Tyr Val Pro Thr
 980 985 990
 Ile Ser His Pro Met Asp Thr Ser Asn Phe Asp Pro Val Asp Glu Glu
 995 1000 1005
 Ser Pro Trp Asn Asp Ala Ser Glu Gly Ser Thr Lys Ala Trp Asp Thr
 1010 1015 1020
 Leu Thr Ser Pro Asn Asn Lys His Pro Glu His Ala Phe Tyr Glu Phe
 1025 1030 1035 1040
 Thr Phe Arg Arg Phe Phe Asp Asp Asn Gly Tyr Pro Phe Arg Cys Pro

12

1045 1050 1055
 Lys Pro Ser Gly Ala Glu Ala Ser Gln Ala Glu Ser Ser Asp Leu Glu
 1060 1065 1070
 Ser Ser Asp Leu Val Asp Gln Thr Glu Gly Cys Gln Pro Val Tyr Val
 1075 1080 1085

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "Y" stands for C or T.
 The letter "N" stands for A, C, G or T.
 The letter "R" stands for A or G.
 The letter "H" stands for A, C or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CAYGTNAARA THACNGAYTT YGG

23

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "R" stands for A or G.
 The letter "D" stands for A, G or T.
 The letter "Y" stands for C or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGRTCDATCA TCCAGCAYTT

20

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Lys Ile Thr Asp Phe Gly
 1 5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Lys Cys Trp Met Ile Asp
 1 5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "R" stands for A or G.
 The letter "D" stands for A, G or T.
 The letter "N" stands for A, C, G or T.
 The letter "S" stands for C or G.
 The letter "W" stands for A or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCCRAACAGD ATNACNCCNA CNSWCCA

27

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "Y" stands for C or T.
 The letter "N" stands for A, C, G or T.
 The letter "M" stands for A or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TTYGGNYTNT GYACNGGNTT YMGNTGG

27

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

14

(A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Phe Gly Leu Cys Thr Gly Phe Arg Trp
 1 5

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Trp Ser Val Gly Val Ile Leu Phe Glu
 1 5

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1088 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met His Pro Ala Gly Glu Lys Arg Gly Gly Arg Pro Asn Asp Lys Tyr
 1 5 10 15
 Thr Ala Glu Ala Leu Glu Ser Ile Lys Gln Asp Leu Thr Arg Phe Glu
 20 25 30
 Val Gln Asn Asn His Arg Asn Asn Gln Asn Tyr Thr Pro Leu Arg Tyr
 35 40 45
 Thr Ala Thr Asn Gly Arg Asn Asp Ala Leu Thr Pro Asp Tyr His His
 50 55 60
 Ala Lys Gln Pro Met Glu Pro Pro Pro Ser Ala Ser Pro Ala Pro Asp
 65 70 75 80
 Val Val Ile Pro Pro Pro Pro Ala Ile Val Gly Gln Pro Gly Ala Gly
 85 90 95
 Ser Ile Ser Val Ser Gly Val Gly Val Gly Val Val Gly Val Ala Asn
 100 105 110
 Gly Arg Val Pro Lys Met Met Thr Ala Leu Met Pro Asn Lys Leu Ile

15

115					120					125					
Arg	Lys	Pro	Ser	Ile	Glu	Arg	Asp	Thr	Ala	Ser	Ser	His	Tyr	Leu	Arg
	130					135					140				
Cys	Ser	Pro	Ala	Leu	Asp	Ser	Gly	Ala	Gly	Ser	Ser	Arg	Ser	Asp	Ser
145					150					155					160
Pro	His	Ser	His	His	Thr	His	Gln	Pro	Ser	Ser	Arg	Thr	Val	Gly	Asn
				165					170					175	
Pro	Gly	Gly	Asn	Gly	Gly	Phe	Ser	Pro	Ser	Pro	Ser	Gly	Phe	Ser	Glu
			180					185					190		
Val	Ala	Pro	Pro	Ala	Pro	Pro	Pro	Arg	Asn	Pro	Thr	Ala	Ser	Ser	Ala
		195					200					205			
Ala	Thr	Pro	Pro	Pro	Pro	Val	Pro	Pro	Thr	Ser	Gln	Ala	Tyr	Val	Lys
	210					215					220				
Arg	Arg	Ser	Pro	Ala	Leu	Asn	Asn	Arg	Pro	Pro	Ala	Ile	Ala	Pro	Pro
225					230				235						240
Thr	Gln	Arg	Gly	Asn	Ser	Pro	Val	Ile	Thr	Gln	Asn	Gly	Leu	Lys	Asn
				245					250					255	
Pro	Gln	Gln	Gln	Leu	Thr	Gln	Gln	Leu	Lys	Ser	Leu	Asn	Leu	Tyr	Pro
				260				265					270		
Gly	Gly	Gly	Ser	Gly	Ala	Val	Val	Glu	Pro	Pro	Pro	Pro	Tyr	Leu	Ile
		275					280					285			
Gln	Gly	Gly	Ala	Gly	Gly	Ala	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Ser	Tyr
	290					295					300				
Thr	Ala	Ser	Met	Gln	Ser	Arg	Gln	Ser	Pro	Thr	Gln	Ser	Gln	Gln	Ser
305					310					315					320
Asp	Tyr	Arg	Lys	Ser	Pro	Ser	Ser	Gly	Ile	Tyr	Ser	Ala	Thr	Ser	Ala
				325					330					335	
Gly	Ser	Pro	Ser	Pro	Ile	Thr	Val	Ser	Leu	Pro	Pro	Ala	Pro	Leu	Ala
			340					345					350		
Lys	Pro	Gln	Pro	Arg	Val	Tyr	Gln	Ala	Arg	Ser	Gln	Gln	Pro	Ile	Ile
		355					360					365			
Met	Gln	Ser	Val	Lys	Ser	Thr	Gln	Val	Gln	Lys	Pro	Val	Leu	Gln	Thr
	370					375					380				
Ala	Val	Ala	Pro	Gln	Ser	Pro	Ser	Ser	Ala	Ser	Ala	Ser	Asn	Ser	Pro
385					390					395					400
Val	His	Val	Leu	Ala	Ala	Pro	Pro	Ser	Tyr	Pro	Gln	Lys	Ser	Ala	Ala
				405					410					415	
Val	Val	Gln	Gln	Gln	Gln	Gln	Ala	Ala	Ala	Ala	Ala	His	Gln	Gln	Gln
			420					425					430		
His	Gln	His	Gln	Gln	Ser	Lys	Pro	Ala	Thr	Pro	Thr	Thr	Pro	Pro	Leu
		435					440					445			
Val	Gly	Leu	Asn	Ser	Lys	Pro	Asn	Cys	Leu	Glu	Pro	Pro	Ser	Tyr	Ala
	450					455					460				
Lys	Ser	Met	Gln	Ala	Lys	Ala	Ala	Thr	Val	Val	Gln	Gln	Gln	Gln	Gln
465					470					475					480

Asp Arg Asp Gly His Ile Lys Leu Thr Asp Phe Gly Leu Cys Thr Gly
 850 855 860
 Phe Arg Trp Thr His Asn Ser Lys Tyr Tyr Gln Glu Asn Gly Asn His
 865 870 875 880
 Ser Arg Gln Asp Ser Met Glu Pro Trp Glu Glu Tyr Ser Glu Asn Gly
 885 890 895
 Pro Lys Pro Thr Val Leu Glu Arg Arg Arg Met Arg Asp His Gln Arg
 900 905 910
 Val Leu Ala His Ser Leu Val Gly Thr Pro Asn Tyr Ile Ala Pro Glu
 915 920 925
 Val Leu Glu Arg Ser Gly Tyr Thr Gln Leu Cys Asp Tyr Trp Ser Val
 930 935 940
 Gly Val Ile Leu Tyr Glu Met Leu Val Gly Gln Pro Pro Phe Leu Ala
 945 950 955 960
 Asn Ser Pro Leu Glu Thr Gln Gln Lys Val Ile Asn Trp Glu Lys Thr
 965 970 975
 Leu His Ile Pro Pro Gln Ala Glu Leu Ser Arg Glu Ala Thr Asp Leu
 980 985 990
 Ile Arg Arg Leu Cys Ala Ser Ala Asp Lys Arg Leu Gly Lys Ser Val
 995 1000 1005
 Asp Glu Val Lys Ser His Asp Phe Phe Lys Gly Ile Asp Phe Ala Asp
 1010 1015 1020
 Met Arg Lys Gln Lys Ala Pro Tyr Ile Pro Glu Ile Lys His Pro Thr
 1025 1030 1035 1040
 Asp Thr Ser Asn Phe Asp Pro Val Asp Pro Glu Lys Leu Arg Ser Asn
 1045 1050 1055
 Asp Ser Thr Met Ser Ser Gly Asp Asp Val Asp Gln Asn Asp Arg Thr
 1060 1065 1070
 Phe His Gly Phe Phe Glu Phe Thr Phe Arg Arg Phe Phe Asp Asp Lys
 1075 1080 1085

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 15:

18

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Ile Ser Lys Pro Ser Lys Glu Asp Gln Pro Ser Leu Pro Lys
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Asp Asp Gln Asn Thr Gly Ser Glu Ile Lys Asn Arg Asp Leu Val Tyr
 1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Pro Ser Gly Lys Asn Ser Arg Asp Glu Glu Lys Arg Glu Ser Arg Ile
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 18:

(2) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

19

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Ser	Asp	Leu	Val	Asp	Gln	Thr	Glu	Gly	Cys	Gln	Pro	Val	Tyr	Val
1				5					10					15

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(51) International Patent Classification ⁶: C12N 15/54, 9/12, 15/11, 15/62, C07K 19/00, 16/40, C12N 5/20, G01N 33/68, A61K 39/00	A3	(11) International Publication Number: WO 99/37787 (43) International Publication Date: 29 July 1999 (29.07.99)
(21) International Application Number: PCT/US99/01145 (22) International Filing Date: 20 January 1999 (20.01.99) (30) Priority Data: 60/072,023 21 January 1998 (21.01.98) US (71) Applicant (for all designated States except US): SUGEN, INC. [US/US]; 230 East Grand Avenue, South San Francisco, CA 94080 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): PLOWMAN, Gregory, D. [US/US]; 4 Honeysuckle Lane, San Carlos, CA 94070 (US). FLANAGAN, Peter [IE/US]; 192 Liberty Street, San Francisco, CA 94110 (US). (74) Agents: WARBURG, Richard, J. et al.; Lyon & Lyon LLP, Suite 4700, 633 West Fifth Street, Los Angeles, CA 90071-2066 (US).	(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims</i> <i>and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 28 October 1999 (28.10.99)	
(54) Title: HUMAN ORTHOLOGUES OF WART (57) Abstract The present invention relates in part to hWART nucleic acid molecules. The invention also relates in part to nucleic acid molecules encoding portions of hWART full-length proteins, nucleic acid vectors containing hWART nucleic acid molecules, recombinant cells containing such nucleic acid vectors, polypeptides purified from such recombinant cells, antibodies to such polypeptides, and methods of identifying compounds that modulate the function of an hWART polypeptide. Also disclosed are methods for diagnosing abnormal cell proliferative conditions in an organism using hWART-related molecules or compounds.		

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CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 99/01145

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/54 C12N9/12 C12N15/11 C12N15/62 C07K19/00
C07K16/40 C12N5/20 G01N33/68 A61K39/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 96 30402 A (UNIV YALE ;XU TIAN (US); TAO WUFAN (US); WANG WEIYI (US); ZHANG SH) 3 October 1996 (1996-10-03) see the whole document, especially SEQ.IDs. 3 and 4	1-16,21, 22
X	EMBL database entry U69566; accession number U69566; 7-Jan-1998; Zollo M. et al.: 'Homo sapiens DRES 7 mRNA sequence. XP002112714 abstract	6,7

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *A* document member of the same patent family

Date of the actual completion of the international search

19 August 1999

Date of mailing of the international search report

09.09.99

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3018

Authorized officer

Mandl, B

INTERNATIONAL SEARCH REPORT

In' tional Application No
PCT/US 99/01145

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBL database entry AA558431; accession number AA558431; 11-Sept-1997; Strausberg R.: 'National Cancer Institute, Cancer Genome Anatomy Project (CGAP).' XP002112713 abstract ---	6,7
A	XU. T. ET AL.: "Identifying tumor suppressors in genetic mosaics: the Drosophila lats gene encodes a putative protein kinase." DEVELOPMENT, vol. 121, 1995, pages 1053-1063, XP002103731 the whole document ---	1-16,21, 22
T	TAO W. ET AL.: "Human homologue of the Drosophila melanogaster lats tumour suppressor modulates CDC2 activity." NATURE GENETICS, vol. 21, February 1999 (1999-02), pages 177-181, XP002103732 the whole document -----	1-16,21, 22

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 99/01145

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 17-20
are directed to a method of treatment of the human/animal
body, the search has been carried out and based on the alleged
effects of the compound/composition.
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such
an extent that no meaningful International Search can be carried out, specifically:
17-20
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all
searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment
of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report
covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is
restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

International Application No. PCT/US 99/01145

Continuation of Box I.2

Claims Nos.: 17-20

Said claims relate to compounds that modulate the function of hWART without giving a further characterization of the claimed matter. In consequence, the scope of said claims is ambiguous and, moreover, their subject-matter is vague and not sufficiently disclosed.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US 99/01145

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-22, partially

A hWART1 polypeptide (as set forth in SEQ.ID.3) or a hWART1 polypeptide lacking specified segments; nucleic acid molecules that encode said hWART1 polypeptide or a hWART1 polypeptide lacking specified segments, nucleic acid molecules that are the complement of said nucleic acid molecules or that hybridize to said nucleic acid molecules; nucleic acid probes for the detection of hWART1 in a sample; nucleic acid molecules encoding fusion proteins that comprise hWART1 or domains of hWART1; recombinant cells comprising nucleic acids encoding hWART1, hWART1 domains or said fusion proteins; antibodies or antibody fragments specific for hWART1; a hybridoma cell producing said antibodies; methods for identifying substances capable of modulating hWART1 activity; a method of preventing or treating an abnormal condition by administering a compound that modulates the function of hWART1; a kit comprising said compound.

2. Claims: 1-22, partially

A hWART2 polypeptide (as set forth in SEQ.ID.4) or a hWART2 polypeptide lacking specified segments; nucleic acid molecules that encode said hWART2 polypeptide or a hWART2 polypeptide lacking specified segments, nucleic acid molecules that are the complement of said nucleic acid molecules or that hybridize to said nucleic acid molecules; nucleic acid probes for the detection of hWART2 in a sample; nucleic acid molecules encoding fusion proteins that comprise hWART2 or domains of hWART2; recombinant cells comprising nucleic acids encoding hWART2, hWART2 domains or said fusion proteins; antibodies or antibody fragments specific for hWART2; a hybridoma cell producing said antibodies; methods for identifying substances capable of modulating hWART2 activity; a method of preventing or treating an abnormal condition by administering a compound that modulates the function of hWART2; a kit comprising said compound.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/US 99/01145

Document search report	Publication date	Patent family member(s)	Publication date
NO 9630402 A	03-10-1996	AU 5431396 A CA 2216702 A EP 0817798 A	16-10-1996 03-10-1996 14-01-1998